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Copyright (c) 1993 - 2003 Compug
SUMMARIES
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Result No.	Score .	Query Match Length DB	ength		ID	Description
_ :	1553	100.0	297	21	AAY71031	Human adenine nucl
2	1553	100.0	297	22	AAU01198	
ω	1553	100.0	297	23	AAU10378	Human adenine nucl
4	1457.5	93.9	298	19	AAW61169	Antl protein. Mus
u	1391.5	89.6	298	21	AAY71032	Human adenine nucl
6	1391.5	89.6	298	22	AAU01199	adenine
7	1391.5	89.6	298	23	AAU10379	Human adenine nucl
8	1385.5	89.2	298	21	AAY71033	adenine
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ALIGNMENTS

RESULT 1
AAY71031
ID AAY7 Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; stroke; MIDD; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; 03-NOV-1998; 08-SEP-1999; Human adenine nucleotide translocator ANT1. 29-AUG-2000 (first entry) AAY71031; AAY71031 standard; Protein; 03-NOV-1999; 11-MAY-2000 W0200026370-A2 Homo sapiens. myoclonic epilepsy red ragged fibre syndrome 98US-0185904 99US-0393441 99WO-US25883 297 A۸

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                     Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                     mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
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                                                                                                                                                                                                                                                                                                                                             ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2001; 2001WO-US15416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; Fig 2; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10378,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10378 standard; Protein; 297
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a recombinant expression construct (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                     present sequence
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS16688
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid
                                                  GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV
                                                                                                 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                               IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                   MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ
                                                                                                                                                                 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                     297
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                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                     AA:
                                                                                                                                                                                                                                                                                                                                     represents the amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clevenger W, Wiley SE, Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translocator 1 (ANT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                 Score 1553; DB 23; Pred. No. 3.2e-173; Mismatches 0;
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                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                    297;
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 240
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RESULT 4
                         Query Match
Best Local
  Matches
                                                                                                                                                                                 The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or gene therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antl: Adenine nucleotide translocator; cloning; screening; DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
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                                                                                                         Sequence
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N-PSDB; AAV36479.
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                                                                                                                                                                independent of
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  279;
                            Similarity
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                                                                                                            298
  Conservative
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                         93.9%;
93.6%;
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  10;
                         Score 1457.5; DB Pred. No. 5e-162;
  Mismatches
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RESULT 5
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                                                                                                                                                                                                                                                                                           Anderson
Ghosh SS;
          The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystdiabeles; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                     Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic against mitochondrial disease \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic;
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                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200026370-A2
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DB; AAD00520.
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                                                                                                                                                          45; Page 172-173; 175pp; English.
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                                                                                                                                                                                                                                                                                                         Davis
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99US-0393441
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 activity, for
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treating diseases
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associated
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                                                                                                                                                                                                                                                                                                                                                           AAU01199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenine nucleotide translocator ANT2 from human brain
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Pred. No. 2.7e
7; Mismatches
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hyperproliferative
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Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; canc Alzheimer's disease; diabetes mellitus; hyperproliferative disorde
                                                                                                                                                                                                 Homo
                                                 03-NOV-2000;
03-NOV-1999;
                                                                                                  10-MAY-2001
                                                                                                                                                WO200132876-A2
                                                                                                                                                                                                                                                                                                                                                                          Human adenine
                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001
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                                                 2000WO-US30535
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                            nucleotide
  99US-0434354
                                                                                                                                                                                                                                                                                                                                                                          translocator-2 (ANT-2)
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disorder survival;

New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.

Murphy AN, Velicelebi

Clevenger G, Davis F

RE;

Wiley

SE,

Andreyev

ΑY,

Frigeri LG

2001-291054/30 DB; AAS05902.

(MITO-) MITOKOR

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RESULT 7
AAULOS AAULO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; adenine mitochondrial m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid % \left( 1\right) =\left\{ 1\right\} =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact
                                                                                                                          11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                             11-MAY-2001; 2001WO-US15416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200185944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10379 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression construct comprising a promoter operably linked to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability
(MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenine nucleotide translocator 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matrix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide translocator; ANT; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; 186pp; English
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Pred. No. 2.7e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ANT2).
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-154;
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N-PSDB; AAS16689
                                                                              MOOS WH,
                                                                              Davis RE,
os WH, Pei
                                                                             Clevenger W,
Y, Carroll /
                                                                              Carroll AK;
                                                                                Wiley SE,
                                                                                Miller SW,
                                                                                 Szabo
                                                                                 7R;
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Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide .

Claim 44; Fig 2; 147pp; English

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid CC comprising an adenine nucleotide translocator (ANT) polypeptide. ANT CC proteins mediate the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide is culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC expressed as a fusion protein with the polypeptide of interest. CC cuseful for identifying an agent that binds to an ANT polypeptide. ANT CC ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is also covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. CC The present sequence represents the amino acid sequence of human ANT2. and

Sequence 298 AA;

Ş Matches Best Local Query Match 263; Similarity Conservative 89.6%; 17; Pred. Score 1391.5; DB 2 Pred. No. 2.7e-154; Mismatches DB 23; 16; Indels Length Gaps

밁 Ş 엉 121 61 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179 120

IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG

120

60

Ş 밁

180 121 180

240 241 297

Вb Ş

181

B Ş

RESULT 8 AAY71033

AAY71033 standard; Protein;

29-AUG-2000

Human adenine nucleotide translocator ANT3:

Human; adenine nucleotide translocator; ANT3; mitochondria: ADP; Avadenosine di-phosphate; adenosine tri-phosphate; appetosis; MPT; c: mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neurol neuroleptic cancer;

Дb

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CC (ANT) proteins or ANT fusion proteins using recombinant expression CC (ANT) proteins or ANT is a nuclear encoded protein and a major component of CC inner mitochondrial membrane. It mediates transport of adenosine CC di/tri-phosphates across the mitochondrial inner membrane and also serves CC as an important molecular component of the mitochondrial permeability CC transition pore, a modulator of apoptosis. ANT is used to identify agents CC or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for CC regulating mitochondrial pore activity, for treating diseases associated CC with altered mitochondrial function, including Alzheimer's, Parkinson's CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic CC epilepsy red ragged fibre syndrome. The present sequence is an accordance of the control of the processor sequence of the control of the control of the present sequence of the control of the control of the present sequence of the control of the control of the present sequence of the control of the control of the present sequence of the control of the control of the control of the present sequence of the control of the control of the present sequence is an accordance of the control of the control of the present sequence of the control of the contr
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant construct encoding adenine polypeptide, useful e.g. in screening f against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1998;
08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 46; Page 173–174; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365619/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000
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                                                                                                 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                            VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPEDTVRRRMMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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99US-0393441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%;
87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clevenger
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Pred. No. 1.4e-153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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stroke; MIDD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller
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241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI

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RESULT 9
AAM39641
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                           Tang
Wang
                                                                                                                                                                                     Zhao
                                                                                                                                                                                                                                                                                                                                                    Alzheimer's; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic; thrombolytic; drug screening; arthritis; i
                                                                                                                                                                         WPI;
                                                                                                                                                                                                                (HYSE-)
                                                                                                                                                                                                                                                 03-AUG-2000;
                                                                                                                                                                                                                                                                                          26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                     WO200153312-A1
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; peripheral nervous system; neuropathy; central nervous system;
                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM39641 standard;
                                                                                                                                                                                                                                                                            21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                               leukaemia.
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DB; AAI58797.
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                                                                                                                                                                                     Liu C
Wang 2
Zhou
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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Wehrman T,
                                                                                                                                                                                     Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                                                                                                           Chen R,
, Xu C,
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                                                                                                                                                                                                                                                                                                                                                       arthritis; inflammation;
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Yang
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                                                                                                                                                                                                                                                                                                                                                             chemotactic;
                                                                                                                                                                                          Ren F,
Zhang
                                                                                                                                                                                                                                                                                                                                                                    haemostatic;
                                                                                                                                                                                                  ,
Li
                                                                                                                                                                                                                                                                                                                                                                           CNS;
                                                                                                                                                                                                  Wang
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Novel nucleic acids and such as central nervous polypeptides, useful system injuries for treating disorders

Example 4; SEQ ID NO 2786; 10078pp; English.

the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Note: The sequence specification. Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and invention relates to The sequen data for human nucleic acids (AAI57798-AAI61369) this patent did not form part of the printed

Sequence 298

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Query Match
Best Local Similarity
Matches 260; Conser 89.2%; 21; Score 1385.5; Pred. No. 1.4e 21; Mismatches 4e-153; DΒ 22; Length 298; **:** Gaps

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RESULT 10
AAUU1200
ID AAUU1200
XX AAUU1
XX AAUU1
XX AAUU1
XX Human
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XX Human
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XX Mitcoc
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The present sequence represents human adenine nucleotide translocator 3 (ANT-3) protein. ANT proteins are mitochondrial permeability transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (c.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transltion pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy AN, Cl
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1999;
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G, Davis R
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mellitus, Parkinson's disease, Huntington's disease, schizophrenia mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
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87.2%;
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Pred. No. 1.4
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Anderson (Ghosh SS, mitochondrial 11-MAY-2000; WO200185944-A2 Human; Human (MITO-) MITOKOR 11-MAY-2001; 15-NOV-2001 sapiens adenine nucleotide translocator 3 (ANT3). adenine A CM, 2000US-0569327 2001WO-US15416 Davis matrix nucleotide translocator; Ŧ, RE, Pei entry) protein Clevenger W, W Y, Carroll AK; Wiley SE, Miller ī ÄS,

Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide

for producing adenine nucl regulated promoter linked

leotide to

Szabo

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N-PSDB;

2002-055598/07

AAS16690

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Best Local S
Matches 260
 21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                       chemokinetic; thrombolytic; drug screening; arthritis; inflammation
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                                                               26-DEC-2000;
                                                                                              26-JUL-2001
                                                                                                                              WO200153312-A1
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                                                                                                                                                                                                                                                                                                       polypeptide SEQ ID NO 6358.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 AA;
2000US-0488725.
2000US-0552317.
2000US-0598042.
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                                                               2000WO-US34263.
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                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                    323 AA
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DEXTX

ABG15423 standard; Protein;

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ABG15423; 18-FEB-2002 Novel human

diagnostic

protein #15414

(first entry)

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RESULT 13
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Best Local S
Matches 260
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assays for receptor activity, arthritis and inflammation, leukaemlas {\tt C.N.S.} disorders.
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                                                                                                                                                                                                                                                                                                                                                                                          Liu C
Wang Z
Zhou
                                                                                                                          QSGRKGADJMYTGTVDCWRKJAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                   QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKV1
                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodrich R,
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87.2%;
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system injuries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1385.5; DB 2
Pred. No. 1.6e-153;
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Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Xue AJ,
C RT;
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Yang Y,
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Zhang
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В
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO of the common of the comm
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 45782; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assobiodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                            IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVHCCCPGXLPYPFDTRSVRRN
                                                                                                                                                                                                                                                                                                                                   MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                               VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSV-TAVAGLLSYPFDT--VRRR
                                                                                                                                                                                                    IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFARNLASG
                                                                                                                                                                                                                                                                                                      MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIIGCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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Pred. No. 7.3e-143;
9; Mismatches 26; 1
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ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII

QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFAGNLASGGAAG QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG AVGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE

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AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE

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RESULT 14
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                                                   specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the Tevelopment of
                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEO ID NO
                                            Sequence
                                                                                                                                                                                                                                     genes from Drosophila and
                                                                                                                                                                                                                                               New isolated nucleic
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                                                                                                (ABB57737-ABB72072)
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                                                                                                                                                                                                   SEQ ID NO 25038; 21pp + Sequence Listing;
Conservative
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           79.9%;
79.7%;
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                                                                                                                                                                                                                                                                                                       PWD,
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 26;
           Score 1241;
Pred. No. 1
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 Mismatches
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           DB 22;
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RESULT 15
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                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB67300 standard; Protein; 299
                                                                                                                             Sequence
                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB67300;
                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 28692; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL11403.
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                                                                                            Similarity
OGFLSFWRGNLANVIRYFPTOALNFAFKDKYKQLFLGGVDRHKOFWRYFAGNLASGGAAG
                                IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK 2/4
                                                                                                                               299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
                                                                                 Conservative
                                                                               79.9%; Score 1241; DB 22; 79.7%; Pred. No. 1.2e-136; tive 26; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                                                                             detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
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                                                                                                     Length 299;
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and cell-cell
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Search completed: June 18, 2003, 13:34:03 Job time: 71 secs

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Title:
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Listing first 45 summaries
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-501-558-2
US-09-234-613-12
US-08-931-878B-56
US-08-518-878B-51
US-08-518-878B-51
US-08-518-878B-51
US-08-68-719A-51
US-08-715-009-32
US-08-775-009-32
US-09-318-199-2
US-09-318-199-2
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ı Similari 19; Cons	1-871-10 2ce 10, Application US NO. 6013858 AL INFORMATION: LICANT: Wallace, Dou LICANT: MacGregor, G Greenlee, TREET: 5370 Manhatta TYY: Boulder TYPE: Floppy d DMPUTER: LBM PC comp PERATING SYSTEM: PC- DTWARE: PATENTION LOTA DMPUTER: JBM PC comp PLICATION NUMBER: U LING DATE: 31-OCT-1 LASSIFICATION UMBER: U LING DATE: 31-OCT-1 LASSIFICATION NUMBER: U LING DATE: 31-OCT-1 LASSIFICATION NUMBER: U LING DATE: 31-OCT-1 LASSIFICATION NUMBER: U LING DATA: PLICATION NUMBER: U LING DATA: PCLETANT: (303) 499-80 AATION FOR SEQ ID NO: LEPAX: (303) 499-80 SCHEFAX: (303) 499-80 SCHEFAX: 298 amino acids DOLOGY: Inear SCULE TYPE: protein	
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FastSEO for Windows Version 3.0
SEO ID NO 339
LENCTH: 469
TYPE: PRT
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Local Similarity 28.9%;
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                                                                                    396
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                                                                                                                                                                                                                                                          284 LVAGSLAGAIAQSSIYPMEVLKTRMAL----RKTGQYSGMLDCARRILAKEGVAAFYKGY 339
                                                                                                                                                                                                                                                                                                                                             234 IREGGAKSLWRGNGINVLKIAPESAIKFMAYEQMKRLV--GSDQETLRIHER-----
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                                                                                                                                                                                                                                                                                                                                                                     62 PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYFAGN 116
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YVVYENLK 461
                                          LVLYDEIK 294
                                                                                    YPLALVRTRMQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSIS 453
                                                                                                                           YPFDTVRRRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFV- 286
                                                                                                                                                                     IPNMLGIIPYAGIDLAVYETLKNTWLQRYAVNSADP---GVFV-LLACGTISSTCGQLAS
                                                                                                                                                                                                             NVSVQGIIIYRAAYFGVYDTAKGM------LPDPKNVHIFVSWMIAQSVTAVAG-LLS
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; Pred. No. 2.4e-26;
64; Mismatches 103; Indels
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; ORGANISM: HOMO SAPIENS US-09-160-119-2

Query Match

18.78;

Score

291;

ВG ۵.

Length

SOFTWARE: FastSEO for Windows Version SEO ID NO 2 LENGTH: 674 TYPE: PRT

EARLIER APPLICATION NUMBER: EP 98401655. EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4

CURRENT APPLICATION NUMBER: US/09/160,119A CURRENT FILING DATE: 1998-09-24 EARLIER APPLICATION NUMBER: EP 97402511.6 EARLIER FILING DATE: 1997-10-23

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US-09-160-119-2
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GENERAL INFORMATION:
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                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                    Sequence 2, Application US/09160119A
Patent No. 6316219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 18.7%; Score 291; DB 4; Length 447; Best Local Similarity 27.5%; Pred. No. 3.2e-25; Matches 80; Conservative 53; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
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APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 YPLDFARTRL - AADV - GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 FGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY
                                                                                                                                                                                                                                                                                                                    328 QTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYPFDTVRRRMMMQSGRKGA
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Gaps

163

218

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CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2000-02-09
NUMBER OF SED ID NOS: 4
SOFTWARE: FASTSEQ for Windows Ver
SED ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
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    RESULT 6
US-08-933-750C-12
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Matches 80; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zambrowicz, Brian APPLICANT: Sands, Arthur T.
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                                                                                                      242 G-RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAMSNVLR-GMGGAFVLVLVDEIKK 295
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                                                                                                                                                                                                                                  122 TIANPTDVLKIRMQA----QSNTIQGGMIGNFMNIYQQEGTRGLWKGVSLTAQRAAIVVG
                                                                                                                                                                                                                                                                    129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                              233 VLRDGRCSGYTGTLDCLLQTWKNEGFFALYKGFWPNWLRLGPWNIIFFVTYEQLKK 288
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                                                                                                                                                                                                                                                                                                                                                  69 SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
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                                                                                                                                                        VELPVYDITKKHLILSGLMGDTVYTHFLSSF-----TCGLAGALASNPVDVVRTRMMNQR 232
                                                                                                                                                                                                                                                                                                              ALYSGIAPAMLRQASYGTIKIGTYQSLKRLF---IERPED--ETLPINVICGILSGVISS
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                                                                                                                                                                                            AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAG-LLSYPFDTVRRRMMMQS 241
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28.48;
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3; Mismatches
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Best Local :
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IMMEDIATE SOURCE:
LIBRARY: SPLNNC
CLONE: 207452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0356
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
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CITY: Palo Alto
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236 RMMM---QSGRK--GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVL
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                                                                                                                                  136 VHPVDVLRTRFAA---QGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAPTLIAIFPYAGLQ 192
                                                                                                                                                        131 VYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAAY 190
                                                                                                                                                                                                              80 KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
                                                                                                                                                                                                                                                                                          20 VAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQEEGPTAFW
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    Application US/08933750C
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                                                        FSCYSSLK------HLY-KWAIPAEGKKNENLQNLLCGSGAGVISKTLTYPLDLFKK
                                                                                            FGVYDTAKGMLPDPKNVH1FVSWM1------AQSVTAVAGLLSYPFDTVRR
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Bandman, Olga
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; LIBRARY: SPLN;
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US-09-234-613-12
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SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234.613
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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PRIOR APPLICATION DATA:
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CITY: Palo Alto
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ZIP: 94304
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    131 VYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAAY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                              KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
                                                                                    RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCF 130
                                                                                                                              VAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQEEGPTAFW 79
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Bandman, Olga
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                                                                                                                                                                                                                                  15.3%; Score 238; DB 4; Length 320
23.5%; Pred. No. 2.8e-19;
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                 Sequence 56, Application US/08518878B Patent No. 5702902 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILLNG DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILLNG DATE: 1997-03-05
EARLIER FILLNG DATE: 1997-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lee James He APPLICANT: Kelly Paine
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TYPE: PRT
ORGANISM: HOMO SAPIEN
      APPLICANT:
                                                                                                                                                                          247
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                                                                                                                                                                                                                                                                                                                                                                                                                              77 PYNGLVAGLQRQMSFASIRIGLYDSVKQVYTPKGADNSSLTTRILA-----GCTTGAMAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 FLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEK--QYKGIIDCVVRIPKEQGFLS 69
                                                                                                                                                                        ---NSPPGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKR 299
                                                                                                                                                                                                                                                                                                                                            TCAQPTDVVKVRFQASIHLGPSRSDRKYSGTMDAYRTIAREEGVRGLWKGTLPNIMRNAI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FWRGNLANVIRYFPTQALNFAFKDKYKOLFL-GGVDRHKQFWRYFAGNLASGGAAGATSL 128
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Tartaglia, Louis A.
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Pred. No. 9e-19;
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US-08-470-868A-56

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                                                                                                                                          Patent No. 5861485
GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Pennie and Edmonds STREET: 1155 Avenue of the Americas
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US-08-518-878B-51
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Best Local S
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                                                                                                                                                                                                                   GENERAL INFORMATION:
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NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
                                                                                                                                APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIO
TITLE OF INVENTION: TREATMENT O
NUMBER OF SEQUENCES: 57
                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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CLASSIFICATION:
COUNTRY: U.S.A. ZIP: 10036-2711
                                   STREET: 1155 Ave
CITY: New York
STATE: New York
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STRANDEDNESS: sir
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                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                          234 -NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 286
                                                                                                                                                                                                                                                                                                                                                                                                    243 RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 SLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHAS----IGSRLLAGSTTGALAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 FLAGAVAAAVSKTAVAPIERVKLLLQVQHASK---QISAEKQYKGIIDCVVRIPKEQGFL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
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                                                                            1155 Avenue
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(212) 869-8864
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                                                                                               Pennie & Edmonds
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                                                                                                                                                       COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
                                                                              of the Americas
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Pred. No. 4.8e-18;
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242

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

OBESITY

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                               STREET: 1155 Ave
CITY: New York
STATE: New York
                                                APPLICATION NUMBER: US/08/807,861A FILING DATE: 26-FEB-1997
                                                                                                                                                                                              ZIP: 10036-2711
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TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01 FILING DATE: 23-AUG-1995
 APPLICATION NUMBER:
                                 CLASSIFICATION:
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IVENTION: METHODS AND COMPOSITIONS FOR THE

IVENTION: REGULATION OF BODY WEIGHT DISORDI
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US 08/518,878
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Pred. No. 5e-18;
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                                                                                                      Version #1.30
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Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartag
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Best Local
                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
              CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              STREET: 1155 A
                                                APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                            STATE: New York
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                                                                                                                                                                                                                                                             1155 Avenue of the Americas
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                 Tartaglia, Louis C.
VERVION: Compositions and Methods for the
VERVION: Treatment of Body Weight Disorder
EQUENCES: 56
                                                                                                                                                                                                                                                                                Pennie and Edmonds
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06-JUN-1995

US/08/470,868A

Floppy disk

Body Weight Disorders, Including Obesity

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TELEFAX: (212) 869-97-
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/294,522 FILING DATE: 23-AUG-1994 ATTORNEY/AGENT INFORMATION:
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LENGTH: 309 amino acids
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STRANDEDNESS: sir
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                                                                                              192 AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM----
                                                                                                                                          189 AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSG 242
244 -NSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEOLKR 296
                                              243 RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                             132 AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC
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Pred. No. 5e-18;
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Patent No. 6057109
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                     APPLICATION NUMBER: FILING DATE: 26-FE APPLICATION NUMBER:
                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
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                                                                                                                                                                                                     APPLICATION NUMBER:
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 FILING DATE:
                 APPLICATION NUMBER:
                                    FILING DATE:
                                                     APPLICATION NUMBER:
                                                                          FILING DATE:
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Similarity 23.8%;
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VENTION: METHODS AND COMPOSITIONS FOR THE
VENTION: REGULATION OF BODY WEIGHT DISORDI
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                                                                                             26-FEB-1997
                        umber: US 08/470,868
06-JUN-1995
                                                                  23-AUG-1995
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23-AUG-1994
                                                                                         US 08/518,878
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Pred. No. 5e-18;
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US-08-946-719A-51
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Best Local Similarity
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                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                 STATE: New York
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                                                                                                                               CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                 APPLICATION NUMBER: US 0 FILING DATE: 23-AUG-1995
                                                                           FILING DATE:
                                                                                                                                                       FILING DATE:
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FILING DATE:
                   APPLICATION NUMBER:
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(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tartaglia, Louis A.
VENTION: COMPOSITIONS FOR THE TREATMENT AND
VENTION: DIACNOSIS OF BODY WEIGHT DISORDERS
EQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                 US 08/470,868
                                                     US 08/518,878
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Pred. No. 5e-18;
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                                                                                                                                                                                                            Version #1.30
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ATIONMET COURTS.

NAME: COTUZZI, LAUTA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEY : 66141 PENNIE

INFORMATION FOR SEO ID NO: 51:

SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-946-719A-51
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Search completed: June 18, 2003, 13:28:53 Job time: 17 secs
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Best Local Similarity 23.88
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/294,522 FILING DATE: 23-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                               243 RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                            192 AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM---- 243
                                                                                                                                                                                                                     189 AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSG 242
                                                                                                                                                                                                                                                                      132 AVAOPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC 191
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                                                                                       244 -NSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEOLKR 296
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Minimum DB seq
Maximum DB seq
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Perfect score:
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350.5
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89.2 8
89.2 8
47.3 3
47.3 22.5 9
22.5 9
22.3 1
19.6 6
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/cgn2_6/ptodata/2/pubpaa/YCCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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10 US-09-810-644-33

10 US-09-801-368-252

10 US-09-734-569-170

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  US-09-992-598-289
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US-10-063-547-58
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                      Sequence 31, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 252, Appl
Sequence 159, App
Sequence 1459, App
Sequence 2, Appli
Sequence 3, Appli
Sequence 289, 1
Sequence 289, 1
Sequence 58, A
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us-10-227-693-58	US-10-063-598-58	US-10-063-518-58	US-09-997-573-289	US-09-997-514-289	US-09-991-172-289	US-09-991-157-289	US-09-998-156-289	US-09-990-437-289	-09-98	-711	US-09-997-666-289	US-09-997-428-289	US-09-990-562-289	US-09-990-438-289	US-10-063-502-58		-616-	653-		687-	-181-	-436-		US-09-990-444-289	US-09-989-735-289
Sequence 58, Appl	-	•		289			289	Sequence 289, App	289	Sequence 289, App	289	Sequence 289, App	Sequence 289, App	_	Sequence 58, Appl		58,							Sequence 289, App	

ALIGNMENTS

RESULT 1 US-09-185-904A-31

GENERAL INFORMATION: APPLICANT: Anderso

APPLICANT: Davis, Robert E.

Clevenger, William Anderson, Christen M.

APPLICANT:
APPLICANT:

Sequence 31, Application US/09185904A Patent No. US20020177185A1

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APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Scabo, Tomas R.
APPLICANT: Scabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANT
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
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Best Local Similarity
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                                    121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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                                                                                               61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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; ORGANISM: Homo sapien
US-09-811-094-31
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US-09-811-094-31
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SOFTWARE: FastSEO for Windows Version
SEO ID NO 31
LENGTH: 297
                                                                                                      GENERAL INFORMATION:
                                                                                                                   Sequence 31, Application US/09810644 Patent No. US20020012992A1
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             APPLICANT:
APPLICANT:
APPLICANT:
                                                                        APPLICANT: Anderson, APPLICANT: Davis, R
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CURRENT FILING DATE: 2001-03-14
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Pei, Yazhong
                           Clevenger, William Wiley, Sandra Eileen Willer, Scott W.
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Willer, Scott W.
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 Soumitra S.
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Pred. No. 2e-157;
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US-09-185-904A-32
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SEQ ID NO 32
LENGTH: 298
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                                                        Query Match
Best Local
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LENGTH: 297
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Best Local
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/185,904A CURRENT FILING DATE: 1998-11-03 NUMBER OF SEQ ID NOS: 33
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Ghosh, Soumitra S.
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                                           Conservative
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                                                       Score 1391.5; DB 9
Pred. No. 3.4e-140;
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Pred. No. 2
                                          Mismatches
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RESULT 6
US-09-810-644-32
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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APPLICANT:
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CURRENT FILING DATE: 2001-03-14
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Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pei, Yazhong
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CURRENT FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 37
SOFTWARE: FastSEO for Windows Version 3.0
SEO ID NO 32
LENGTH: 298
TYPE: PRT
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                                                                      CURRENT APPLICATION NUMBER: US/09/185,904A CURRENT FILING DATE: 1998-11-03 NUMBER OF SEQ ID NOS: 33
                                                                                                                        TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING TITLE OF INVENTION: THEREFOR FILE REFERENCE: 660088.420
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ORGANISM: Homo sapien
                LENGTH: 298
TYPE: PRT
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Ghosh,
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Wiley, Sandra Eileen
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                                                             for Windows Version
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US-09-811-094-33
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Best Local Similarity 87.2
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LENGTH: 298
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APPLICANT: Wiler, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AN TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088, 42004
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 37
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87.2%;
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               APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: NO. US20020128:
APPLICANT: Royer, John
APPLICANT: Royer, John
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
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LENGTH: 298
                                                                                                                                                                                                        Sequence 252, Application US/09801368 Patent No. US20020128250A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILLING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 37
SOFTWARE: FastSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IPKEQGFLSFWRGNLANVIRYFPTOALNFAFKDKYKQLFLGGVDRHKOFWRYFAGNLASG
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Similarity 87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                   Maxon, Mary
Milne, Todd
No. US20020128250Alman,
                                                                                        Holtzman, Doug
Madden, Kevin
Royer, John
Salama, Sof
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TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. US20020064816A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170
                                                            SEQ ID NO 170
                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                              TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASE-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR PPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
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                                                                            SOFTWARE: PatentIn Ver.
                                                                                                NUMBER OF SEQ ID NOS: 18:
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ORGANISM: Physcomitrella
                                    ENGTH: 386
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nes 156; Conserv
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                                                                                                                                                                                                                                                                         Duwenig, Elke
Schmidt, Ralf-
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                                                                                                                                                                                                                                                     Reski, Ralf
                                                                                                                                                                                                                                                                                                               Freund, Annette
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Ehrhardt, Thomas
Reindl, Andreas
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                                                                            1/WordPerfect
  patens
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Matches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1459, Application US/09925301 Patent No. US20020052308A1
                                                                                                       Matches
                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (126)
OTHER INFORMATION:
                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (129)
                                                                                                                                                                                                                                                      OTHER INFORMATION:
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156; Conserv
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                                                   26
                         61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRH 106
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Pred. No. 6.6e-70;
                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                     any
                                                                                                                  Score 461; DB 1
Pred. No. 2e-41;
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US-09-864-761-36440
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Annomax Sequence Listing Engine SEQ ID NO 36440 LENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36440, Application US/09864761
                                                                                                                                                                                   OTHER INFORMATION: 10
OTHER INFORMATION: 10
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OTHER INFORMATION: 10
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Cheh, Wensheng
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                 TYPE: PRT.
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                     FEATURE
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FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27 APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
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      INFORMATION:
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                                     IN HEART, SIGNAL = 2.2
IN HELA, SIGNAL = 7.3
IN BT474, SIGNAL = 2.7
IN ADDLT LIVER, SIGNAL = 1.1
IN BRAIN, SIGNAL = 2
                                                                                                                                           IN FETAL LIVER, SIGNAL = 2.3
IN BONE MARROW, SIGNAL = 1.5
IN PLACENTA, SIGNAL = 1.9
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      AW935235.1,
    EVALUE 6.00
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                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HD TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CL001103

CURRENT FAPLICATION NUMBER: US/09/777,921A

CURRENT FILLING DATE: 2002-02-07

NUMBER OF SEO ID NOS: 126
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FastSEQ

for Windows Version 4.0

HUMAN TRANSPORTER PROTEIN

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RESULT 15
US-09-777-921A-2
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US-09-777-921A-4
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Sequence 2, Application US/09777921A Patent No. US20020115136A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ISOLATED : TITLE OF INVENTION: AUCLEIC A TITLE OF INVENTION: AND USES FILE REFERENCE: CL001103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MERKULOV et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 47
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSN---VLRGMGGAFVLVLYDEIKK 295
                                                                                                                                                                                   359 DLAVYELLKSHWLDNFAKDSVNPGVLVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
                                                                                                                                                                                                                                                                                            130 FVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAA
                                                                                                                                                                                                                                                                                                                                248 LWRGNGTNVIKIAPETAVKFWYYEQYKKLLTEEGQKIGTFERFISGSM-----AGATAQT
                                                                                                                                                                                                                                                                                                                                                                                                        196 RQLLAGGIAGAVSRTSTAPLDRLKVMMQV-HGSKSMNIFGGFRQMI-----KEGGVRS
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76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 22.6%;
l Similarity 32.3%;
95; Conservative 5
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                                                                                                          GAPQL -- NMVGLFRRIISKEGLPGLYRGITPNFMKVLPAVGISY -- VVYENMKQ
                                                                                                                                                                                                                     YFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 350.5; DB 10; Length Pred. No. 7.1e-29; 55; Mismatches 115; Indels
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Pred. No. 2e-35;
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LENGTH: 477;
TYPE: PRT;
ORGANISH: Homo sapiens
US-09-777-921A-2
Search completed: June 18, 2003, 13:32:46 Job time: 25 secs
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.3%; Score 346.5; DB 10; Length 477; Best Local Similarity 32.7%; Pred. No. 1.9e-28; Matches 96; Conservative 55; Mismatches 116; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                              421 GSPQL--NMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY--VVYENMKQ 470
                                                                                             245 GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSN---VLRGMGGAFVLVLYDEIKK 295
                                                                                                                             361 DLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420
                                                                                                                                                                                             190 YFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK 244
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OM protein - protein search, using sw model
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June 18, 2003, 13:32:22; Search time 40 Seconds (without alignments) 713.798 Million cell updates/sec
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Title: Perfect score: Sequence:

US-09-393-441-31 1553 1 MGDHAWSFLKDFLAGAVAAA.....LRGMGGAFVLVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29 737	28 740	7	744	25 745.5	745	746	746	751	752	752	756	770	7	15 904.5	14 973.5		1037.	1043.	_		1368.	.0	.5	:	4 1458.5	ω.	66.	1 1526.5		No. Score	Result
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				386								308				300 :			313 2					298 1		298 2		298		Length DB	
1 S29852	2 S14874			2 \$17917										2 S51132	2 A41677	-	2 T25371				2 S31814		S0389			2 S37210		1 A44778	;	ВID	
ADP,ATP carrier pr	ADP, ATP carrier pr	tical pro		ADP, ATP carrier pr	carrier	ATP	transloc	carrier	ADP, ATP carrier pr	hypothetical prote	carrier	٠.				tical pro	carrier	carrier	carrier	carrier	carrier	ADP, ATP carrier pr	carrier	nucleoti	ADP,ATP carrier pr		Description				

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327	334.5	345.5	349.5	350.5	363	367.5	368	508	676	718.5	728.5	729	733.5	734	736	
21.1	21.5	22.2	22.5	22.6	23.4	23.7	23.7	32.7	43.5	46.3	46.9	46.9	47.2	47.3	47.4	
332	348	358	352	475	381	325	415	327	298	309	306	305	313	318	307	
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T47703	D84798	T45934	T01729	T50686	T51158	T04273	T48171	T51577	T24029	A24849	T42011	S68154	XWNC	A31978	A36582	
Ca-dependent solut	probable mitochond	hypothetical prote	mitochondrial solu	peroxisomal Ca-dep	hypothetical prote	hypothetical prote	hypothetical prote	ADP/ATP translocas	hypothetical prote		•		ADP, ATP carrier pr	ADP, ATP carrier pr	ADP,ATP carrier pr	

ALIGNMENTS

C;Genetics: A;Gene: GDB:ANT1; :T1 A;Cross-references: GDB:119680; OMIM:103220 A;Cross-references: GDB:119680; OMIM:103220 A;Cross-references: GDB:119680; OMIM:103220 A;Map position: 4q35-4q35 C;Superfamily: ADP,ATP carrier protein; ADP.ATP carrier protein C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein E;2-298/Product: ADP,ATP carrier protein #status predicted <mat> F;2-298/Product: ADP,ATP carrier protein repeat homology <acp1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <acp2></acp2></acp1></mat>	A; MOLECUJE Type: MRKM A; MOLECUJE CYPE: MRKM A; Residues: 1-15, /A v,17-146, /RR', 149,151-226, /L', 228-298 <nec> A; Residues: 1-15, /A v,17-146, /RR', 149,151-226, /L', 228-298 <nec> A; Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920 A; Experimental source: clone pHMANT R; Houldsworth, J.; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988 A; Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA 16 A; Reference number: A94197; MUID:88124845; PMID:2829183 A; Accession: A28116 A; Molecule type: mRNA A; Residues: 1-37 <houy a;="" cross-references:="" experimental="" gb:j03593;="" liver<="" nid:g339724;="" pid:g339725="" pidn:aaa36751.1;="" source:="" th=""><th>A;Molecule type: DNA A;Residues: 1-298 <coz> R;Residues: 1-298 <coz> R;Neckelmann, N; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C. R;Neckelmann, N; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C. Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987 A;Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of A;Reference number: A39891; MUID:88041149; PMID:2823266 A;Accession: A39891 A;Status: preliminary</coz></coz></th><th>A; Residues: 1-298 <lia> A; Residues: 1-298 <lia> A; Residues: 1-298 <lia> A; Cross-references: GB.J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659 A; Cross-references: GB.J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659 A; Cross-references: GE.J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659 A; Title: DNA sequences of two expressed nuclear genes for human mitochondrial AE A; Reference number: S03893; MUID:89236396; PMID:2541251 A; Accession: S03893 A; Stalus: not compared with conceptual translation</lia></lia></lia></th><th>RESULT 1 A44778 A44778 ADP,ATP carrier protein T1 - human ADP,ATP carrier protein T1 - human N;Alternate names: mitochondrial ADP,ATP translocase 1 C:Species: Homo Sapiens (man) C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C;Accession: A44778; S03893; A39891; A29116 R;Li, K:, Warner, C.K:, Hodge, J.A.: Minoshima, S.; Kudoh, J.; Fukuyama, R.; Mae J. Biol. Chem. 264, 13998-14004, 1989 J. Biol. Chem. 264, 13998-14004, 1989 A;Title: A human muscle adenine nucleotide translocator gene has four exons, is A;Reference number: A44778; MUID:89340499; PMID:2547778 A;Accession: A44778 A;Status: preliminary</th></houy></nec></nec>	A;Molecule type: DNA A;Residues: 1-298 <coz> R;Residues: 1-298 <coz> R;Neckelmann, N; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C. R;Neckelmann, N; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C. Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987 A;Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of A;Reference number: A39891; MUID:88041149; PMID:2823266 A;Accession: A39891 A;Status: preliminary</coz></coz>	A; Residues: 1-298 <lia> A; Residues: 1-298 <lia> A; Residues: 1-298 <lia> A; Cross-references: GB.J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659 A; Cross-references: GB.J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659 A; Cross-references: GE.J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659 A; Title: DNA sequences of two expressed nuclear genes for human mitochondrial AE A; Reference number: S03893; MUID:89236396; PMID:2541251 A; Accession: S03893 A; Stalus: not compared with conceptual translation</lia></lia></lia>	RESULT 1 A44778 A44778 ADP,ATP carrier protein T1 - human ADP,ATP carrier protein T1 - human N;Alternate names: mitochondrial ADP,ATP translocase 1 C:Species: Homo Sapiens (man) C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C;Accession: A44778; S03893; A39891; A29116 R;Li, K:, Warner, C.K:, Hodge, J.A.: Minoshima, S.; Kudoh, J.; Fukuyama, R.; Mae J. Biol. Chem. 264, 13998-14004, 1989 J. Biol. Chem. 264, 13998-14004, 1989 A;Title: A human muscle adenine nucleotide translocator gene has four exons, is A;Reference number: A44778; MUID:89340499; PMID:2547778 A;Accession: A44778 A;Status: preliminary
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298

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adenine nucleotide translocator - rat C:Species: Rattus norvegicus (Norway rat) C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #t. C:Accession: 160173  
R:Shinohara, Y:: Kamida, M.: Yamazaki, N:: Terada, H. Blochim. Blochim. 1152, 192-196, 1993 A:Title: Isolation and characterization of cDNA clone: A:Reference number: 160173; MUID:94002161; PMID:83993 A:Accession: 160173
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A:Introns: 37/3; 200/1; 247/1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Superfamily: ADP,ATP carrier protein protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                           GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
OSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                   GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS 180
                                                                                                                                                                                                                  IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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Pred. No. 1.6e-130;
2; Mismatches 2;
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PMID:8399300
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A; Molecule type: mRNA
A; Residues: 208-298 < RAS>
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A; Residues: 1-298 <LAP>
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120

120

240

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C:Keywords: duplication: transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: adenine nucleotide carrier C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan C;Accession: S37210
                                                                                                                                                                                                                                                                                           C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP,ATP carrier protein Tl -
                    1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                              Conservative
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                                                                                                                                            Score 1463.5;
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                                                                                              Mismatches
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                                                                                                                     No. 8e-125;
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                                                                                              Indels
                                                                                                                                            Length 298;
                                                                                                                                                                                                                                                                                        protein
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                                                                                              Gaps
60
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R:Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two
A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822 C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-ul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bowline genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808 ADP,ATP carrier protein T1 - bovine N;Alternate names: ADP/ATP translocase C;Species: Bos primigenius taurus (catt A;Residues: 1-298 <POW>
A;Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1; 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS VQGI1IYRAAYFGVYDŢAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM VOGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM 239 GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTK1FKSDGLKGLYQGFSVS 7 distinct mRNAs and PID:9529415 expressed differe 297 298

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R:Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier A;Reference number: A29132; MUID:87166056; PMID:3031073
A;Accession: A29132
                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A29132; C28116
                                                                                                                                                                     ADP,ATP carrier protein T2 - human N;Alternate names: mitochondrial ADP,ATP translocase C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                             RESULT
A29132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Oettmeler, W.; Masson, K.; Kalinna, S.
Eur. J. Blochem. 227, 730-733, 1995
A;Title: [(3)H]7-azido-4-isopropylacridone
A;Reference number: S69369; MUID:95172058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: residue 52 may be methyllysine R: Babel, W: Wachter, E: Aquila, H: Kling. Biochim. Biophys. Acta 670, 176-180, 1981 A; Title: Amino acid sequence determination A; Reference number: A61343; MUID:82046808; A; Accession: A61343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Note: located in the inner mitochondrial membrane C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid: F:5-99/Domain; ADP,ATP carrier protein repeat homology <ACP1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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Pred. No. 2.3
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PMID:7867632
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R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116
                                                                                                                                                                                                                                                                                                                                               R:Cozens, A.L.: Runswick, M.J.: Walker, J.E.
J. Mol. Biól. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes for human A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Accession: S03894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP.ATP carrier protein T3 - human

N;Alternate names: ADP.ATP carrier protein T2 (misi

C;Species: Homo sapiens (man)

C;Date: 17-Mar-2000.#sequence_revision 17-Mar-2000

C;Accession: S03894; B28116
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A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;Cross-references: GB.J03591; NID:g339720; PIDN:AAA36749.1;
A;Experimental source: clone pHAT3
C;Genetics:
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed A:Reference number: A94197; MUID:88124845; PMID:2829183
A:Accession: C28116
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A; Residues: 1-298 <BAT>
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A; Residues: 1-298 <COZ>
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A; Molecule type: mRNA A; Residues: 36-104, "R', 106, 'A', 109-298 <HOU> A; Cross-references: GB:J03592; NID:g339722; A; Experimental source: liver C; Genetics:

PIDN: AAA36750.1;

PID:9339723

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A:Gene: GDB:ANT3; ANT3Y
A:Gene: GDB:ANT3; ANT3Y
A:Gross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Morposition: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein F:2-298/Product: ADP,ATP carrier protein fstatus predicted <AMT> F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F:10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F:10-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Keywords: duplication; homousmer; microscope <ACP1>F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Residues: 1-298 <POW>
A; Cross-references: GB: M24103; NID: 9529416; PIDN: AAA30769.1; PID: 9529417 A; Cross-references: GB: M24103; NID: 9529416; PIDN: AAA30769.1; PID: 9529417 C: Superfamily: ADP, ATP carrier protein; MITO-MOND CONTROL PROTEIN ATP CAPTION ATP CAPTION ATP CAPTION ATPONNATION AND APPLY 
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                                                                                 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                              IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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Pred. No. 2.6
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Pred. No. 9.1e-118;
1; Mismatches 16;
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A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier C;Keywords: duplication; transmembrane protein
E;7-101/Domain: ADP,ATP carrier protein repeat homology

protein repeat homology

A:Reference number: S31935 A:Accession: S31935 A:Status: preliminary

ADP.ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936
C;Baccession: S31935; S31936
C;Baccession: S31935; S31936
C;Accession: S319

#text_change 10-Sep-1999

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RESULT S31935

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A:Molecule type: mRNA
A:Rosidues: 1-298 <COS>
A:Cross-references: EMBL:X70847
A:Cross-references: EMBL:X70847
C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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S31814
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N;Alternate names: adenine nucleotide t
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan 1995 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                             GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
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               QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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87.2%;
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8; Mismatches 19;
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hypothetical protein T01B11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
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A;Residues: 1-313 <GEI>
A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
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R; Geisel, C.; Stellyes,
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A; Introns: 4/1; 191/2
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A;Accession: T25850
A;Status: preliminary; translated from GB/EMBL/DDBJ
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F;209-300/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP:T01B11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                    TSLCFVYPLDFARTRLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
                            DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                               AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA
                                                                                                                                          LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRMMMOSWPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDG11GLYRGFNVSVQG11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                                                                                           LCFVYPLDFARTRLAADVGKANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGA 125
                                                              AAYFGMFDTAKMVFTADGKKLNFFAAWAIAQVVTVGSGILSYPWDTVRRRMMMQSGRK--
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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ADP, ATP
                                                                                                                                                                                                                                                                                                                                  67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.6%; Score 1142.5; DB 1; 76.2%; Pred. No. 9.1e-96; tive 26; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrier protein repeat homology <ACP2> carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                     36; Mismatches
                                                                                                                                                                                                                                                                                                                                  Score 1045.5; DB 2; Pred. No. 5.8e-87;
                                                                                                                                                                                                                                                                                                                     49;
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313
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A;Map position: 3 A;Introns: 20/1; 41/3; C;Superfamily: ADP,ATP

115/2 carrier protein;

ADP, ATP carrier

protein repeat

homology

Query Match
Best Local Similarity
Matches 201; Conserv

Conservative

38;

66.8%;

Score 1037.5; DB Pred. No. 2.9e-86; 8; Mismatches 49

DB 2; 49;

Indels Length

ω ··

Gaps

A; Gene: CESP:T27E9.1

Genetics:

A; Experimental source: clone T27E9

A; Molecule type: DNA
A; Residues: 1-300 <WIL>
A; Cross-references: EMBL: Z82059; PIDN: CAB04874.1; GSPDB: GN00021; CESP: T27E9.1

GB/EMBL/DDBJ

submitted to the EMBL Data Library, A; Reference number: Z20024

November 1996

R; Lloyd, C.

A; Reference number: A; Accession: T25371

A; Status: preliminary; translated from

hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C:Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #t C:Accession: T25371

15-Oct-1999 #text_change 11-Jan-2000

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A; Map position: 4
A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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C:Date: 15-Oct-1999 #sequence_revision
C:Accession: T23207
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A; Residues: 1-313 <WIL>
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Best Local
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              DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
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DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                                                                                    AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSGRKGA 246
                                                                                                                                                                                                   LCFVYPLDFARTRLAADVGRRAQREFHGLGDC11K1FKSDGLRGLYQGFNVSVQG111YR 187
                                                                                                                                                                                                                                             AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                         FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKG1VDVLVRVPKEQGY
                                                                                                                                                                                                                                                                                                                                                                FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGF
                                                                              AAYFGMFDTAKMVFTADGKKLNFFAAWATAQVVTVGSGIISYPWDTVRRRMMMQSGRK--
                                                                                                                                                            LCFVYPLDFARTRLAADVGKANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                            67.2%;
69.4%;
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A:Map position: 1

A:Map position: 1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology F:9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
ADP,ATP carrier protein - Chlorella kes
C:Species: Chlorella kessleri
C:Date: 30-Jun-1992 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein W02D3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tC;Accession: T15206
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A; Residues: 1-300 <LET>
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A; Accession: T15206
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                                                                                                                                                DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHLI 300
                                                                                                                                                                 DIMYTGTVDCWRK1AKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                             AAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRRMMMQSGRK--
                                                                                                                                                                                                                                                                    AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                             LCFVYPLDFVRTRLGADVGKGVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIYR
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                                                                                                                                                                                                                                                                                                                                                                                            AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAYFGMFDTAKMVFASDGQKLNFFAAWGIAQVVTVGSGILSYPWDTVRRRMMMQSGRK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMDVLIRVPKEQGV 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carrier protein repeat homology
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                                        Chlorella kessleri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1005.5;
Pred. No. 2.3e
0; Mismatches
30-Jun-1992 #text_change
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                   QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
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A:Molecule type: mRNA
A:Residues: 1-339 <HIL>
A:Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
A:Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat tomology <ACP1>
F:38-134/Domain: ADP,ATP carrier protein repeat tomology <ACP2>
F:241-329/Domain: ADP,ATP carrier protein repeat tomology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the A;Reference number: A41677; MUID:92084708; PMID:1748677
A;Accession: A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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-GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKFI 329
                                                               KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
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0: Mismatches 65;
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A:Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335 (C:Superfamily: ADP.ATP carrier protein; ADP.ATP carrier protein repeat home C:Keywords: duplication; transmembrane protein F:6-102/Domain: ADP.ATP carrier protein repeat homology <ACP1>F:112-203/Domain: ADP.ATP carrier protein repeat homology <ACP2>F:209-301/Domain: ADP.ATP carrier protein repeat homology <ACP3> R; Hatin, I.; Jaureguiberry, G Eur. J. Biochem. 228, 86-91, 1995 Eur. J. Biochem. 228, and 1995 A; Title: Molecular characterisation of the A; Reference number: S68993; MUID:95188918; N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 07-May.1995 #sequence_revision 01-Sep-1995 C;Accession: S68993; S51132 A; Molecule type: mRNA A; Residues: 1-301 <HAT> A; Status: preliminary ADP,ATP carrier protein - malaria parasite Similarity NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA--EKQYKGIIDCVVRIPKE Conservative 58.2%; 48; Score 904.5; DB 2; Pred. No. 3.2e-74; "'mmatches 70; ADP/ATP-transporter PMID:7883016 (Plasmodium #text_change Indels Length 301; falciparum) CDNA 09-Jun-2000 5. from homology the 67 64

	Search completed: June 18, 2003, 13:36:47 Job time : 41 secs	Search completed: Job time : 41 secs	Sear Job
	16 :	247	дb
	244 KG-ADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297	244	Q Q
24	187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSYTILAGLISYPFDTVRRRWMMSGE 246	187	дb
243	185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMOSGR	185	0y
18	127 AISLLIVYPLDFARTRLASDIGKGKDROFTGLFDCLAKIYKQTGLLSLYSGFGVSVTGII 186	127	Db
18	125 ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184	125	Оy
12	68 QGVLSLWRCNVANVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILSGATAG 126	68	ф

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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CM protein - protein search, using sw model

Fun on: June 18, 2003, 13:28:56; Search time 22 Seconds (without alignments) 559.930 Million cell updates/sec

Title: Perfect score: Sequence: US-09-393-441-31 1553

1 MGDHAWSFLKDFLAGAVAAA.....LRGMGGAFVLVLYDEIKKYV 297

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters: 112892

אות DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27 729 28 728.5 29 718.5 29 718.5 30 302.5 31 300.5 32 296.5 33 296.5	NO. Score 1 1526.5 2 1466.5 3 1466.5 4 1453.5 6 1408.5 6 1408.5 7 1398.5 9 1385.5 9 1385.5 11 1162.5 12 177.5 13 770.5 14 756.5 16 752.5 16 752.5 17 751.5 18 756.5 19 744.5 20 744.5 21 742.5 22 740.5 23 733.5	Result
46.9 46.3 19.5 19.3 19.1		
305 331 309 678 330 702	Length DB	
ADTZ_KLULA ADTZ_WHEAT ADT1_YEAST CMC1_HUMAN GDC_BOVIN CMC1_CAEEL CMC2_CAEEL	ADT1_HUMAN ADT1_RAT ADT1_BOVIN ADT1_BOVIN ADT2_HUMAN ADT2_HUMAN ADT3_HUMAN ADT3_HUMAN ADT3_HUMAN ADT3_HUMAN ADT1_ANOGA ADT_CHLKE ADT_CHLKE ADT_CHLKE ADT1_MAIZE ADT1_GOSHI ADT1_GOSHI ADT1_MAIZE ADT1_MAIZE ADT1_MAIZE ADT1_MAIZE ADT1_MAIZE ADT1_MAIZE ADT1_MAIZE ADT1_NEATH ADT1_SOLTU ADT1_SOLTU ADT1_SOLTU ADT1_SOLTU ADT1_SOLTU ADT1_NEAT ADT2_VEAST ADT2_VEAST ADT3_YEAST ADT3_YEAST ADT1_REDCR ADT1_REDCR ADT1_REDCR ADT1_REDCR ADT1_NEATH ADT1_SOLTU ADT1_SOLTU ADT1_SOLTU ADT1_SOLTU ADT1_NEATT ADT2_VEAST ADT1_REDCR ADT1_REDCR ADT1_REDCR ADT1_REDCR ADT1_REDCR ADT1_REATT ADT1_NEATT	
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263.5	265.5	266.5	267.5	270.5	279.5	280	286	291	292	292.5	295
17.0	17.1	17.2	17.2	17.4	18.0	18.0	18.4	18.7	18.8	18.8	19.0
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Q9va73 drosophila		Q03028 saccharomyc	Q9z2b2 mus musculu	Q9h1k4 homo sapien	Q9qxx4 mus musculu	Q9h2d1 homo sapien	Q19529 caenorhabdi	09ujs0 homo sapien	P16260 homo sapien	099297 saccharomyc	P16261 rattus norv

ALIGNMENTS

RARRA	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RESULT ADT1_H ADT1_H AD ID PACE PACE PACE PACE PACE PACE PACE PACE	
VARIANTS PEO PRO-114 AND MET-289. WARDLINE-20385067; PubMed-10926541; Kaukonen J., Juselius J.K., Tiranti V., Kyttala A., Zeviani M., Comi G.P., Keranen J., Peltonen L., Suomalainen A.; "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";	SEQUENCE OF 1-37 FROM N.A. TISSUE-Liver; MEDLINE-88124845; PubMed-2829183; HOuldsworth J., Attardi G.; "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver."; Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).	MEDLINE-BROWING. PubMed-2823266; MECKElmann N., Li K., Wade R.P., Shuster R., Wallace D.C.; Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.; "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes."; Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987). SEQUENCE FROM N.A. TISSUE-Eye; Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-89236396; pubMed-2541251; COZENS A.L., Runswick M.J., Walker J.E.; COZENS A.L., Runswick M.J., Walker J.E.; "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase."; J. Mol. Biol. 206:261-280(1989). [2] SEQUENCE FROM N.A. MEDLINE-89340499; PubMed-2547778; MEDLINE-89340499; PubMed-2547778; Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.; Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.; Ta human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed."; J. Biol. Chem. 264:13998-14004(1989).	_HUMAN _ADTI_HMAN STANDARD; PRT; 298 AA. P1235; O1-QCT-1989 (Rel. 12, Created) O1-NOV-1990 (Rel. 16, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updatte) ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1). SLC25A4 OR ANT1. Homo sapiens (Human). Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9806;	

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                                                                                                                                           Matches
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Best Local
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PIR; A44778; A44778.
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PIR; A39891; A39891.
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                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR001993; Mitoch_carrier. Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
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MIM; 157640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DISEASE: Defects in SLC25A4 are a cau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
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             121
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J03593; AAA36751.1; -.
J04982; AAA51736.1; -.
BC008664; AAH08664.1; -.
                                     61
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                                                                                                                                                       Similarity
GAAGATSLCFYYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                   MGDHAMSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                     IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                       MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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147
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                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
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V-> M (IN PEO).

/FIId-var_012112.

G-> A (IN REF. 3).

G-> RR (IN REF. 3).

V-> L (IN REF. 3).
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Pred. No. 2.3e-1
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Query Match
Best Local
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TRANSMEM 12
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TRANSMEM 117
TRANSMEM 176
TRANSMEM 214
TRANSMEM 214
TRANSMEM 273
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Q1-FEB-1994
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                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                           InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and characterization of cDNA clones and a genomiencoding rat mitochondrial adenine nucleotide translocator. Biochim. Biophys. Acta 1152:192-196(1993).

-:- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley, and Wistar; TISSUE-Heart, MEDLINE-94002161; PubMed-8399300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                EMBL; X61667; CAA43842.1; -. EMBL; D12770; BAA02237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinohara Y., Kamida M., Yamazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLC25A4 OR ANT1
                                       SEQUENCE
                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                     REPEAT
                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A L
EXTENT, IN BRAIN AND KIDNEY.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane
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Similarity
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                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                   29
91
134
195
231
291
110
208
94.48;
                                         32989
                                                                                                                                                                                                membrane;
                                         ME.
Score 1466.5; DB 1; Pred. No. 7e-127;
                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                         66704FF78C6BC320 CRC64;
                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Liver;
           Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO A LESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone
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RESULT AND THE RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MOUSE
ADT1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                        "Expression and sequence analysis of translocase 1 and 2 genes.";
Submitted (MAR-2000) to the FMR1 //---
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P48962: 062164;
01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2007 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1
translocase 1) (Adenine nucleotide translocator 1) (ANT 1)
SLC25A4 OR ANT1 OR ANC1.
                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
HITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=97059403; PubMed=8903724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheri
NCBI_TaxID=10090;
[1]
                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laplace C., Costet P.;
Submitted (SEP-1993) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/c; TISSUE-Muscle;
Laplace C., Costet P.;
                      between the
                                                                                                                                                                                            <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mamm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellison J.W.,
                                                                                                                                                                                                                                                                                                                                           TISSUE-Eye;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rapid evolution
                                                                                                                inner membrane.
DOMAIN: COMPOSED OF
SIMILARITY: BELONGS
                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                       SUBUNIT: HOMODIMER
  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQGI11YRAAYFGVYDTAKGMLPDPKNVHJFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X., Francke U., Shapiro I of human pseudoautosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                   THREE HOMOLOGOUS DOMAINS.
TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wallace of the mou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse
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AND ATP ACR
                                                                                                                                                                                            protein.
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                                                                                                                                                                                              Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide
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1) (mANC1).
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EMBL;
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EMBL; BC003791; AAH03791.1; ...
EMBL; BC026925; AAH26925.1; ...
MGD; MGI:1153495; S1c25a4.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                          BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; pF00153; mito_carr; 3.
pRINTS; pR00926; MITOCARRIER:
pR0SITE; pS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                    ADT1_BOVIN
P02722;
                                                                       Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                              (Adenine nucleotide translocator 1) (ANT 1). SLC25A4 OR ANT1.
                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Cre 01-JUL-1993 (Rel. 26, Las 16-OCT-2001 (Rel. 40, Las ADP, ATP carrier protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U27315; AAC52837.1;
X74510; CAA52616.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; family.
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176
214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                           STANDARD;
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134
195
231
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208
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26, Last seq
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                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
in, heart isoform T1 (ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X
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Pred. No. 1.3e-126;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                   Craniata; Vertebrata; Eute
actyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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3A849FEAB0981462 CRC64;
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                                                                                                                                                                                                                                                                                                                           297
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                                                                                                                                                                                                                          translocase
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                                                                                                                                          Euteleostom1;
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MEDLINE-89229093; Powell S.J., Medd SEQUENCE FROM N.A.

PubMed=2540808; S.M., Runswick

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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Bovine cardiac mitochhndrial ADP/ATP-carrier: two an unusually short 3'-noncoding sequence."; Biochem. Biophys. Res. Commun. 138:850-857(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict the produced by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 138:85
-!- FUNCTION: CATALYZES THE EXCHANGE
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A43646; A43646.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M13783;
EMBL; M24102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-82188267; PubMed-7076130;
Aquila H., Misra D., Eulitz M., Klingenberg No. (Complete amino acid sequence of the ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Two bovine differences
                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rasmussen U.B., Wohlrab H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86295775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 207-297 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoppe-Seyler's 2. Physiol. Chem. 363:345-349(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A03181;
A24822;
                                                                                                                                                                                                                                           280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inner membrane
                        123
                                                                   62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00926; MITOCARRIER. PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                             Similarity
AGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQ
                                                                                                                                                                   DHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIP
                                                              KEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGA
                                                                                       KEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGA
                                                                                                                                                 DQALSFLKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes for mitochondrial ADP/ATP
in various tissues.";
                                                                                                                                                                                                                                           Conservative
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A24822.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane;
                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=3017341;
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133
194
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297
                                                                                                                                                                                                                                                        93.6%;
94.6%;
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                                                                                                                                                                                                                                    Score 1453.5; DB 1
Pred. No. 1.1e-125;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                            - 6 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOCKED
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                                                                                                                                                                                                                                                                                                                         A582D3C4A40AEB48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
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                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                    Gaps
                    181
                                                              121
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RESULT 5
ADT2_MOUSE
                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             "Expression and sequence analysis o
translocase 1 and 2 genes.":
EMBL; U27316; AAC52838.1; EMBL; U10404; AAA19009.1; EMBL; X70847; CAA50196.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P51881; Q61311;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
ADP, ATP carrier protein, fibroblast isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS.
Laplace C.;
Submitted (FEB-1997) to
                                                                                                                                                                                                                                                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20432087;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Costet P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
                                                                                                                                                                                                                                 ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheldon J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Rapid evolution homologs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLC25A5 OR ANT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellison J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADT2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (1995),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Adenine nucleotide translocator
                                                                                                                                                                                                         DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                    MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                    EUNCTION: CATALYZES
                                                                                                                                                                                                                                                  inner membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FEB-1993)
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ion of human pseudoautosomal gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University
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                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10974536;
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Rodentia;
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fibroblast isoform (
slocator 2) (ANT 2).
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                                                                                                                                                                                                                                                                                                                    EXCHANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                        of.
                                                                                                                                                                                                                                                               membrane protein.
                                                                                                                                                           It is produced through a collaboration informatics and the EMBL outstation .
                                                                                                                                                                                                                                                                                                                                                                      Wallace
f the mou
                                                                                                                                                                                                                                                                                                                    QF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes
                                                                                                                                                                                                                                                                                                                    AND
                                                                                                                                                                                                                                                                                                                                                                                         D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADP/ATP
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                                                                                                                                                                                                                                                                                                                   ATP
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                                                                                                                                                                                                                                                                                                                   ACROSS
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                                                                                                                                                                                                                                                                 Mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                      nucleotide
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                                                                                                                                       outstation -
lions on its
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RESULT 6
ADT2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 266; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT2_RAT

ADT2_RAT

ADT2_RAT

ADT2_RAT

STANDANU;

O09973;

O1-FEB-1995 (Rel. 31, Created)

O1-FEB-1995 (Rel. 31, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

ADP_ATP carrier protein, fibroblast isoform

ADP_ATP carrier protein p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
REPEAT
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                                                                          STRAIN-Sprague-Dawley; TISSUE-Liver;

MEDLINE-94002161; PubMed-8399300;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

"Isolation and characterization of cDNA clones are encoding rat mitochondrial adenine nucleotide training for the straining of the straini
                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Adenine nucleotide translocator SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER
                                                   -!- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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  inner membrane
TISSUE SPECIFIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPKEQGELSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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  SPECIFICITY: PRESENT
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32931 MW;
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Pred. No. 1.4e
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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hes 13;
BRAIN,
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                                                protein. Mitochondrial
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                                                                                                                                                                                          translocator
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HEART,
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                                                                                                                                                                                       genomic ocator.";
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AND
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Eukaryota; Metazoa; Mammalia; Eutheria;

s (Human).
s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (

Catarrhini; Craniata;

Hominidae;

Vertebrata; Euteleostomi;

SLC25A5 OR ANT2

(Adenine nucleotide translocator

2) (ANT

2)

(ADP/ATP

۵

Homo sapiens

SEQUENCE FROM N. TISSUE-Placenta;

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RESULT 7
ADT2_HUMAN
ID ADT2_H
AC P05141
AC P05141
DT 13-AUG
DT 01-OCT
DT 15-JUN
DE ADP,AT
DE (Adeni
GN SLC25A
OS Homo s
OC Eukary
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Best Local S
Matches 266
                                                                                         ADT2_HUMAN STANDARD: PRT: 298 AA. P05141; 043350; 13-AUG-1987 (Rel. 05, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ADP,ATP carrier protein, fibroblast isoform () ADP,ATP carrier translocator 2) (ANT 2).
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REPEAT
REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D12771; BAA02238.1; InterPro; IPR002067; Mit_carrier. InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-slb.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKELETAL MUSCLE.
                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                              QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                                                                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYOGFNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
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Pred. No. 1.7e.
16; Mismatches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M57424; AAA51737.1; -. EMBL; J02683; AAA35579.1; -. EMBL; L78810; AAB39266.1; -. EMBL; AC004000; AAB96347.1; -.
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InterPro; IPR001993; Mito
Pfam; PF00153; mito_carr;
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      CONFLICT
                       CONFLICT
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MIM; 300150; -
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Mazzarella R.A., Schlest
Submitted (JUN-1996) to
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"Two distinct genes for ADP/ATP translocase level in adult human liver.";
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MEDLINE-87166056; PubMed-3031073;
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J. Biol Chom To The Communication of the Biol Chom To The Communication of the Biol Chom To The Communication of the Biol Chom To The
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SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integral membrane
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DOMAIN: COMPOSED OF THI
SIMILARITY: BELONGS TO
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to the EMBL/GenBank/DDBJ
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TO THE MITOCHONDRIAL CARRIER FAMILY
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Best Local
      Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
-!- SUBUNIT: HOMODIMER.
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CONFLICT
SEQUENCE
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01-0CT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, liver isoform T2 (ADP/ATP (Adenine nucleotide translocator 3) (ANT 3).
SLC25A6 OR ANT3.
                                                                                                                                    TISSUE-Brain,
Strausberg R.;
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Zhou J., Yu W., Tang
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SEQUENCE FROM N.A.
MEDLINE=89236396; PubMed=2541251;
MEDLINE=89236396; PubMed=2541251;
Malke
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Eukaryota; Metazoa; (
                                                     Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are level in adult human liver.";
                                                                                    MEDLINE-88124845; PubMed-2829183;
                                                                                              TISSUE-Liver;
                                                                                                                           Submitted
                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                   Zhou J., Yu W.
Margolin J.F.;
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                           Houldsworth J.,
                                                                                                         SEQUENCE
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RESULT 9
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EMBL; AY007135; AAG01998.1; -.
EMBL; BC007295; AAH07295.1; -.
EMBL; BC007850; AAH07850.1; -.
EMBL; BC008935; AAH08737.1; -.
EMBL; BC008935; AAH0835.1; -.
EMBL; BC014775; AAH14775.1; -.
        ADT3_BOVIN
P32007;
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 01-JUL-1993 (Rel. 26, Created)
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                                           QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                    QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
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IPR001993; Mitoch_carrier.
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3 KHTO -> RHA (IN REF. 4).
5 -> F (IN REF. 3; AAH1477.
4 No. 1.8e-119;
7 matches 16
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Mammalia; Eutheria;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- FUNCTION: CATALYZES THE EXCHANGE OF MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP, ATP carrier protein, in nucleotide translocator 3)
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InterPro: IPR001993; mitoch_carrier.

    -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

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                                                                             IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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Pred. No. 5.1e-119;
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P/ATP translocase
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Belson K.M., Bouch J., Borokstein P., Brottler P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,

RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Mesherson D.L.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shee B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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Q26365; Q26254; P91614; Q9VZ70;

15-JUL-1998 (Rel. 36, Lreated)

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT) (Stress sensitive B protein).

SESB OR A/A-T OR CG16944.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Peterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilia.

MCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang Y.Q., Davis A.V
Submitted (JAN-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Berkeley;
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"Molecular analysis of a candidate isolation between sibling species of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94350065; PubMed-7520869;
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of Drosophila.";
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AVGFVKDFAAGQVSAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE

QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFAGNLASGGAAG

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EMBL; S71762;
EMBL; Y10618;
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"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: S71762; AAB31734.3; -. EMBL: Y10618; CAA71628.1; -. EMBL: AE003484; AAF47957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inner membrane (By similarity).

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER (BY SIMILARITY)
                         S
                                                                                                Similarity
AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00215;
                                                                                                                                                                                                                        14
75
119
177
214
272
18
18
81
200
266
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB23114.1; -
                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCH_CARRIER;
                                                                                                                                                                                                                     31
93
136
196
231
290
200
266
                                                                                                78.0%;
79.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane;
                                                                                                                                                                                       GOTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

OV -> GI (IN REF. 3 AND 4).

I -> Y (IN REF. 1).

R -> RG (IN REF. 3 AND 4).

G -> A (IN REF. 2).

PC -> TGA (IN REF. 3 AND 4).

C -> S (IN REF. 1).
                                                                                                                                                                          ₹
₹
                                                                         25; Mismatches
                                                                       Pred. No. 1.6e·103;
5; Mismatches 33;
                                                                                                                     Score 1211;
                                                                                                                                                                     AA639439968F9750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat: Tran (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                  Length 297;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE
                                                                       <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ons on its in no way commercial
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                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _ANOGA
                                                                                                                                                                                                                                                                                   TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: L11618; AAB04104.1; -
EMBL: L11617; AAB04105.1; -
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Colicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insect Mol. Biol. 3:35-40(1994).
-!- FUNCTION: CATALYZES THE EXCHANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gambiae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94348635; PubMed=8069414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP,ATP carrier protein (ADP/ATP translocase) translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADT_ANOGA
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                        Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beard C.B., Crews-Oyen A.E., Kumar V.K., "A cDNA encoding an ADP/ATP carrier from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane
185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK
                                                                                                                                                                                                                                                                                                                                                                                               PF00153; mito_carr;
                                                                                                                                          8
                                                                                                                                                                     6
                                                                                                                                                                                                               Similarity
                                                                                 TSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFNVSVQGII
                                         TSLCFVYPLDFARTRLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
                                                                                                                                                       WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQ
                                                                                                                                         YGFAKDFLAGGISAAVSKTAVAPIERVKLLLQVQAASKQIAVDKQYKGIVDCFVRIPKEQ
                                                                                                                                                                                                                                                         301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                        Inner membrane;
                                                                                                                                                                                                                                                                                   31
93
136
197
233
                                                                                                                                                                                                              74.98;
                                                                                                                                                                                                                                                         32863 MW;
                                                                                                                                                                                               26;
                                                                                                                                                                                                                           Score 1162.5;
                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                           Repeat; Transmembrane; (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                         4CC9E17C9F8DA08B CRC64;
                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins F.H.;
the mosquito Anopheles
                                                                                                                                                                                                               .5e-99
                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diptera; Nematocera;
                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pancrustacea; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                          Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                                                                                                 1:
                                                                                                                                                                                                 Gaps
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ADT_CHLKE
JD ADT_CA
AC P3169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Glucose increases the expression of the glyceraldehyde-3-phosphate dehydrogenase J. Biol. Chem. 266:24044-24047(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translocator) (ANT).
Chlorella kessleri.
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M76669; AAA33027.1; -. PIR; A41677; A41677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92084708; PubMed-1748677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlorellaceae; Chlorella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADT_CHLKE
                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - ! - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00153;
                                                                                                                                              40
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
                                                QGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLAG
                                                                                           QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
                                                                                                                                                 AFVKDLLAGGTAGAISKTAVAPIERVKLLLQTQDSNPMIKSGQVPRYTGIVNCFVRVSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002067; Mit_carrier.
IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                             339 AA;
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mito_carr; 3.
6; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        126
168
228
265
                                                                                                                                                                                                                                                                      62.7%;
65.3%;
                                                                                                                                                                                                                                                                                                                                             36686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlorophyta; Trebouxiophyceae;
                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                        Score 973.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                             54779734A33B3942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Transmembrane;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                      o
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339
                                                                                                                                                                                                                                                                      le-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP/ADP translocator and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ⋛
                                                                                                                                                                                                                                                                                             DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translocator gene from Chlamydomonas rei
Mol. Gen. Genet. 237:134-144 (1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharpe J.A., Day A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translocator) (ANT).
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01-AUG-1992 (Rel. 23, Last seq
01-OCT-1994 (Rel. 30, Last ann
                                                                                                                                                                                                                                                                                                                                       Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X65194; CAA46311.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93204887; PubMed-8455552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FUD44-R2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
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                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane.
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                                                                                                            Similarity
                                    SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ
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33528 MW;
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Last annotation update
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Pred. No. 3.4e
19; Mismatches
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D477CF0E72B7A53F CRC64;
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                                                                            3.4e-63;
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP.ATP carrier protein 1, mitochondrial precursor translocase 1) (Adenine nucleotide translocator 1)
ANTI OR ANT-G1.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                         Leaver C.J., Bathgate B., Baker A.;
"Two genes encode the adenine nucleotide translocator of maize mitochondria. Isolation, characterisation and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                   Winning B.M., Day C.D., Sarah C.J.
"Nucleotide sequence of two cDNAs
translocator from Zea mays L.";
Plant Mol. Biol. 17:305-307(1991).
                                                                                                                                                       Nucleic Acids Res. 13:5857-5867(1985).
                                                                                                                                                                                                                 MEDLINE-85297781; PubMed-2994015;
Baker A., Leaver C.J.;
                                                                                                                                                                                                                                                                                       structural genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MUTIND-FR7205034;
MEDLINE=91322533; PubMed=1863785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays (Maize)
                                                                                                                                                                                     translocator of Zea mays L
                                                                                                                                                                                              "Isolation and sequence analysis of a
                                                                                                                                                                                                                                             SEQUENCE OF 70-387 FROM N.A.
                                                                                                                                                                                                                                                                                                                                            MEDLINE-89338399; PubMed-2547608;
                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV
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                                                                                                              SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION:
                                                                    SIMILARITY: BELONGS
                                                                                   DOMAIN: COMPOSED OF THREE HOMOLOGOUS
                                                                                                  inner membrane.
                                                                                                                                            MITOCHONDRIAL INNER MEMBRANE
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                                                                    TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                              Integral
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yta; Liliopsida; Poales; Poaceae; PACC clade;
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                                                 ADT_SCHPO STANDARD: PRT: 322 AA 009188; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ADP,ATP carrier protein (ADP/ATP translocator) (ANT). ANCI OR SPBC530.10C.
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Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                         MMOSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEI----
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53.8%;
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Pred. No. 8.4e
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-> Y (IN REF. 3).
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RA WOOD V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Holgson G.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Weltjens J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens J., Vonstreels E., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gereuth A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golibert F., Aves S.J., Xiang Z., Hunt C., Mooree K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G. V., Ussery D., Barrell B.G., Nurse P.;
The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880 (2002).

CC. --- Fillowski G. V., Ussery D., Barrell B.G., Nurse P.;

CC. --- Fillowski G. V., Ussery D., Barrell B.G., Pand Arp Across THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.; "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation
                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.";
Gene 171:113-117(1996).
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                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inner membrane.
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848401; PubMed=11859360;
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InterPro; IPR001993; Mitoch_carrier.
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AL023634; CAA19176.
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Scoring table:
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Perfect score:
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Copyright (c) 1993 - 2003 Compugen Ltd
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044093 drosophila
044094 drosophila
062526 drosophila
025129 halocynthia
029h0c2 homo sapien
                                                          Q95vx4 ethmostigmu
Q9nhw5 lucilia cup
Q95s30 drosophila
Q91336 rana sylvat
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Q9yic4 rana rugosa
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A Yamaguchi N., Kasai M.;

T regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle.";

L J. Biochem. 335;541-547(1998).

C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

C INNER MEMBRANE (BY SIMILARITY).

C INNER MEMBRANE (BY SIMILARITY).

REMBL; AB009386: BAA23777.1;

RICTPRO: IPR001993; Mitoch_carrier.

PR InterPro: IPR002067; MIT_CCARRIER.

DR Pfam; PF00153; mito_carr; 3.

PROSITE: PS00215; MITOCH_CARRIER: 3.

PROSITE: PS00215; MITOCH_CARRIER: 3.
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Best Local
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                          SEQUENCE
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Similarity
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Last annotation updat
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                                                                                                                                             Score 1464.5; DB 6; Length 298; Pred. No. 6.2e-126; 7; Mismatches 8; Indels 1;
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                      Query Match
Best Local
  Matches
                                                                                                                                           EMBL: X74510: CAA52616.1; -...
EMBL: AF240002: AAF64470.1; -...
EMBL: BC003791: AAH03791.1; -...
EMBL: BC003791: AAH03791.1; -...
EMBL: BC0036925: AAH26925.1; -...
MGD: MGI:1353495: SIc25a4.
InterPro: IPR001993: Mitoch_carrier.
InterPro: IPR002067: Mit_carrier.
Pfom: PF00153: mito_carr: 3.
PRINTS: PR00926: MITOCARRIER.
PROSITE: PS00215: MITOCH_CARRIER: 3.
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062164;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide translocator), member 4) (Hypothetical 32.9 kDa protein).
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STRAIN-BALB/C; TISSUE-MUSCLE;
Laplace C., Costet P.;
                                                                               Hypothetical protein; Inno
Transport; Mitochondrion.
SEQUENCE 298 AA; 32904
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-EYE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Expression and sequence analysis of the mouse
translocase 1 and 2 genes.";
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Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                     INDITITED (APR-2002) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE MITOCHONDETA.
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                   Similarity
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  Conservative
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                      94.2%;
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                                                                                                                         Inner membrane; Repeat; Transmembrane;
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Score 1463.5; DB 1: 
Pred. No. 7.7e-126; 
0; Mismatches 7;
                                                                                    3A849FEAB0981462 CRC64;
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Best Local :
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01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Yamazaki N., Shinohara Y., Tanida K., Terada H.;
"Structural properties of mammalian mitochondrial ADP/ATP carriers:
identification of possible amino acids that determine functional
differences in its isoforms.";
Mitochondrion 1:371-379(2002).
EMBL; AB065433; BAB84673.1;
  Q9YIC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenine nucleotide translocator 2.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Bovidae; Bovinae; Bos.
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
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PRELIMINARY;
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Pred. No. 4.4e-121;
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  PRT;
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298
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298; 1:

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Mol. Biol. Evol. 15:1612-1619 (1998)

C -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

C -: SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

REMBL; AB008457: BA36507.1; --

RINterPro; IPR001993; Mitoch Carrier.

RINterPro; IPR002030: Mit_uncoupling.

REMBL; PR00153; mito_carr; 3.

REMBL; PR00155; MITOCH_CARRIER.

REMBL; PR00185; MITOCH_CARRIER.

REMBL; PR00185; MITOCH_CARRIER.

REMBL; PR00185; MITOCH_CARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2002 (TEEMBLrel. 20,
                                                                                                                                        Rana rugosa (Wrinkled frog).
Eukaryota: Metazoa: Chordata:
Amphibia: Batrachia: Anura: No
                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
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Amphibia; Batrachia;
  SEQUENCE FROM N.A.
MEDLINE-99083429; PubMed-9866197;
Miura I., Ohtani H., Nakamura M.,
"The origin and differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99083429; PubMed=9866197;
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                                                                                                                                                                                                           ADP/ATP translocase
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                                                                                                                                                                                                                                                                                                                                Q9PRH1
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"The origin and differentiation of the heteromorphic sex chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8410;
                                                                                                                  NCBI_TaxID=8410;
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NCE 298 AA; 33068 MW; 15B270ED37099A00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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i H., Nakamura M., i differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
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                                                                                                                                        Chordata; Craniata; Vertebrata; Anura; Neobatrachia; Ranoidea;
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Last sequence up
Last annotation
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Last annotation updat
                                                                                                                                                                                                                                                                                   Created)
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Pred No. 5.7e
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    Ichikawa Y., Saitoh
f the heteromorphic s
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Ranidae; Rana
                                                                                                                                          Euteleostomi;
Ranidae; Rana
    sex
       chromosomes
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MEDLINE-9908429; PubMed-9866197;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

The origin and differentlation of the heteromorphic sex chromosomes

of a continuous form of the heteromorphic sex chromosomes

of a sex-linked gene, Anp/ATP translocase.*;

of a sex-linked ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY

R EMBL; ABOO8463; BAA36506.1; -.

R EMBL; ABOO8461; BAA36501.1; -.

R EMBL; ABOO8461; BAA36511.1; -.

R EMBL; ABOO8462; BAA36512.1; -.

R EMBL; ABOO8462; BAA36512.1; -.

R InterPro; IPR001993; Mitoch_carrier.

R InterPro; IPR002067; Mit_carrier.

R InterPro; IPR002067; Mit_carrier.

R InterPro; IPR002030; Mit_uncoupling.

R Pfam; PF00153; Mito_Carr; 3.

R PRINTS; PR00926; MITOCARRIER.

R PRINTS; PR00784; MITOCH_CARRIER; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.

O SEQUENCE 298 AA; 33054 MW; BOE23AD56F548D36 CRC64;
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Best Local Similarity
Matches 258; Conserv
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Amphibia; Batrachia; Anura; Neobatrachia;
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana rugosa (Wrinkled frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP/ATP translocase
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Pred. No. 5.7e-118;
Pred. No. 5.7e-118;
                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
eobatrachia; Ranoidea; Ranidae; Rana
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Best Local S
Matches 257
                                                                               INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CALEMBL; AF231347; AAR63471.1; -.

InterPro: IPR001993; Mitoch_carrier.

InterPro: IPR002067; Mit_carrier.

InterPro: IPR002030; Mit_uncoupling.

Pfam; PF00153; mito_carrier.

PfINTS: PR001926; MITOCARRIER.

PRINTS: PR001926; MITOCARRIER.

PRINTS; PR001926; MITOCH_CARRIER; 3.

Inner membrane; Mitochondrion; Transmembrane; T:

SEQUENCE 298 AA; 32940 MW; 91B740133751877F
                                     Matches
                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversag "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Sp "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Sp Dynamic Patterns of Expression During Development.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MIT
                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Creat 01-OCT-2000 (TrEMBLrel. 15, Last 01-MAR-2002 (TrEMBLrel. 20, Last
                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
NCB1_TaxID+8355;
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q919M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane; Mitochondrion; Transmembrane; Transport. SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;
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PRINTS: PR00784; MTUNCOUPLING.
PROSITE: PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002030; Mit_uncoupling
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                Adenine nucleotide translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                              919M9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQG11IYRAAYFGVYDTAKGMLPDPKNVHJFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM 239
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                              88.0%;
                                    23;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                   Score 1366.5; DB 1: 
Pred. No. 5.8e-117; 
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                Transmembrane; Transpor
91B740133751877F CRC64;
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annotation
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                                                          DB 13;
                                                                                                                                                                                                   CARRIER FAMILY
                                                                                            Transport
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                                                        Length
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Specific a
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Best Local
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Q9NHW5;
Q9NHW5;
Q1-QCT-2000
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01-DEC-2001
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF401758; AAL02100.1; -
InterPo; IPR001993; Mitoch_carrier.
Piam; PF00153; mito_carr; 3.
PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 299 AA; 33037 MW; 3C3BBCBZ6E7C3C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Pleurostigmophora; Scolopendromorpha; Scolopendridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP-ATP translocator. Ethmostigmus rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of an ADP-ATP translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=62613;
                               244 KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIYRAAYEGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPEDTVRRRMMMQSGR
                                                                                                                                                                                                                                                                IIYRAAYFGTYDTAKGMLPDPKNTPIVISWLIAQTVTTCAGIISYPFDTVRRRMMMQSGR
                                                                                                                                  ATSLCFVYPLXFARTRLAADIGKGLEQREFTGLGNCIAKIFKSDGLVGLYRGFGVSVQGI
                                                                                                                                                 ATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI
                                                                                                                                                                                                  QGILSYWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFLGNLASGGAAG
                                                                                                                                                                                                                   QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
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                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                  80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         Score 1245.5; DB 5; DE 19...
Pred. No. 7e-106;
""" and takes 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      3C3BBCB26E7C3C5E CRC64;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Ward C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INNER MEMBRANE (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE MITOCHONDRIAL
EMBL; AF218587; AAF32322.1; --
Interpro: IPR001993; Mitoch_carrier.
Interpro: IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Z., Fair J.A., Batterham P.;
"A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Encaheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                 095S30;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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Lucilia cuprina (Greenbottle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                      GM12886p (LP02726p).
SESB OR CG16944.
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                                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASGGAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASGGAAGATSLCFVYPLDFARTRLAADTGKGGQREFTGLGNCLAKIFKSDGLVGLYRGFG
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                                                                                                                         Brokstein
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Pred. No. 1.6e
25; Mismatches
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la; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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annotation update)
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ches 36;
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                                                                                                                                                                                                                                               Brachycera; Muscomorpha;
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C.J.,
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Patel S., Phouanenavong S.,
Celniker S.;
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SEQUENCE
                                                                                                                                                                                                                    MEDLINE-97398141; PubMed-9256066; Cai Q., Greenway S.C., Storey K.B.; Cai Fernial regulation of the mitochondrial in wood frogs under freezing stress."; Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91336;
Q91336;
                                                                                                         Cai Q., Storey K.B.;
Submitted (APR-1999) to the
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; No
NCBI_TaxID-45438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2002 (TrEMBLrel. 20, ADP/ATP translocase.
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Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL; AY060978; AAL28526.1; EMBL; AY070894; AAL48516.1; FlyBase; FBgn0003360; sesB.
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana sylvatica (wood frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL EMBL: U44832; AAA97882 2;
                                                                                                                                                          TISSUE-LIVER;
  InterPro;
                                                 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MISTINEER MEMBRANE (BY SIMILARITY).
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  IPR001993;
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79.78;
Mitoch_carrier
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Last sequences the control of the control 
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Neobatrachia; Ranoidea;
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Pred. No. 1.8e
Pred. Mismatches
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1.8e-105;
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-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL: AF025798; AABB7883.1;
-F1yBase: F8gn0023292; Dpse\sesB.
Interpro; IPR001993; Mitoch_carrier.
Interpro; IPR002067; Mit_carrier.
Interpro; IPR002067; Mit_carrier.
Pfam: PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCH_CARRIER.
PROSITE: PS00215; MITOCH_CARRIER: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00926; MITOCARRIER. PROSITE; PS00215; MITOCH_CARRIER; 3. Inner membrane; Mitochondrion; Trans.
                                                                                                                                                                                                                                                                               Zeng L.-W., Comeron
Genetica 0:0-0(1997)
                                                                                                                                                                                                                                                                                                                                           Drosophila pseudoobscura (Fruit fly).
Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tachtera; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                              Ephydroidea; Dro
NCBI_TaxID=7237;
                                                                                                                                                                                                                                                                                                                                                                                              SESB.
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Pfam; PF00153; mito_carr; 3.
                                                                                                                        SEQUENCE
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                                                                                                                                              nner membrane; Mitochondrion;
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                                                                                   Similarity
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QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
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                                                                                                                       31725 MW;
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79.68;
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                                                                         25;
                                                                                  Score 1183; DB 5;
Pred. No. 3.5e-100;
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Pred. No. 7.6
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                                                                                                                                              Repeat; Transmembrane;
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Best Local S
Matches 226
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER EMBL: AF025799; AAB87884.1: -

EMBL: AF025799; AAB87884.1: -

F1yBase: FBgn002237; Dsub\sesB.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.

InterPro; IPR002067; Mit_carrier.

Pfam; PF00153; mito_carr; 3.

PRINTS: PR00926; MITOCARRIER.

PROSITE: PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SESB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inner membrane; Mitochondrion;
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226; Conser
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GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLV :|:| |: || ||| || |||||:||||||| ATEIIYKNTIHCWGTIAKQEGT-AFFKGAFSNVLRGTGGAFVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMOSGRK
                                                                                                                                                                                        ATSLCFVYPLDFARTRLAADTGKGGQREFTGLGNCLTK1FKSDGLVGLYRGFGVSVQG11
                                                                                                                                                                                                                 ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
                                                                                                                                                                                                                                                                                                       QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                               AMGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                        AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1183; DB 5;
Pred. No. 3.5e-100;
3; Mismatches 33;
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Query Match
Best Local Similarity
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                                                                                                                                                 FlyBase; FBgn002511; Ant2.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR09926; MITOCARRIER; UNKNOWN_2.
PROSTTE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 307 AA; 33744 MM; 3D6B3DFD82061COC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANT2 protein.
ANT2 OR CG1683.
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AEO03484; AAF47956.1; -.
EMBL; Y10618; CAA71629.1; -.
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(TremBLrel. 07, Last sequence update)
(TremBLrel. 17, Last annotation update)
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     73.
     Score 1147; DB 5; Pred. No. 7.5e-97;
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                                              Length 307;
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RESULT 15
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Best Local
                                                                                                                                                                     Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                       Miya T., Makabe K., Satoh N.;
"Expression of a gene for major mitochondrial translocase, during embryogenesis in the ascic
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123 AGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQG
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                                             KEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGA 122
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                                 KEOGFFSLWRGNLANVIRYFPTQALNFAFKDTYKKIFLAGVDKRKQFWRYFHGNLASGGA
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Search completed: Job time : 83 secs	Db	νo	ОЮ	07	D¦5
omple : 83	243	243	183	183	123
Search completed: June 18, 2003, 13:36:01 Job time : 83 secs	243 RNKEDRMYKGTVDCWGKIYKNEGGKAFFKGALSNVIRGTGGALVLVLYDELKKLV 297	243 RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297	183 IIVYRAAYFGTYDTVKGMLPDPQNTPIIVSWAIAQVVTTGAGIISYPFDTVRRRMMMQSG 242	183 IIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSG 242	123 AGATGLCFVYPLDFARTRLAADIGSGGSRQFTGLGNCLATIVKKDGPRGLYQGFVVSIQG 182

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SUMMARIES

SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AX134718 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		NN G	ហហហ	ហ្ស	54			ហូហូ	51 (n UI UI U	J UJ UJ UJ D OD OD O	5 5 4 5 6 4	75	75	77	,		Result No. Sc
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rtebrata; Hominidae; reyev,A.Y.	linear PAT 2		AC110340 Ra AC130772 Ra AC130777 Ra	AB008459 Ra AB008450 Ra AB008458 Ra	AB008456 R AB008461 R AB008457 R	D12771 Ra AB008462 R AB008463 R	BC004570 Mu U27316 Mus	AX301847 Se U10404 Mus J02683 Huma	M24103 BOV AF231347 X	BC008737 H AB065433 B	AY007135 H BC007850 H BC014775 H	BC031912 H BC008935 H	027315 Mu AX134720 S	BC003791 x74510 M.	D12770 Ra BC026925	M24102 Bov	BC008664 H	AX134718 Si AX301846 Si	Descriptio
Euteleostomi; Homo. , Frigeri,L.G.,	9-MAY-2001		Mus muscu Rattus no Rattus no Rattus no		Rana rugo Rana rugo Rana rugo	Rattus norv Rana rugo Rana rugo	- 6 2	equence s musculu an ADP/A	Bovine ADP/ 47 Xenopus 1	Homo sapi Bos tauru	Homo sapi	omo sapi	Sequence	Mus muscu musculus	Rattus norv 25 Mus muscu	ine ADP/	564 Homo sapi	Sequence Sequence	

Velicelebi, G. and Davis, R.E.	REFERENCE 1 (bases 1 to 894) AUTHORS Murphy, A.N., Clevenger, W., Wiley, S.E., Andreyev, A.Y., Frigeri, L.G.,	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	KEYWORDS SOURCE human.		AX134718 LOCUS AX134718 B94 bp DNA linear PAT 29-MAY-2001 DEFINITION Sequence 1 from Patent WOO132876.	RESULT 1
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                                                                                                                                                            TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA
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CTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCAGAGTGTGACG
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AX301846
Sequence 1 from
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Szabo, T.R., Ghosh, S.S., Moos, W.H., Pei, Y. and Carroll
Production of adenine nucleotide translocator (ant),
ligands and screening assays therefor
Patent: WO 0185944-A 1 15-NOV-2001;
                                                                                                                                                                   MITOKOR (US)
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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224 c 26
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                                                                                                                  /organism="Homo sapiens"
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Patent WO0185944.
                 0.0%;
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                                                                                      267
Score 894; DB b; ...
Pred. No. 3.2e-180; ...
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Query Match Best Local Matches 89	BASE COUNT	CDS	gene	FEATURES Source	PUBMED COMMENT	JOURNAL	REFERENCE AUTHORS TITLE	ORGANISM	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 3	da Ko	Q Y	0 y	0y Db	da
y Match 100.0%; Score 894; DB 9; Length 1320; Local Similarity 100.0%; Pred. No. 3.1e-180; hes 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0; hes 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 ATGGGTGATCACGCGTTGGAGCTTTCCTAAAGGACTTCCTGGCCGGGGGGGG	/translation="McDHAWSFLKDFLAGAVARYKTANAPIERVKLLLOVOHASKO ISAEKOYKGIIDCVVRIPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGG VDRHKOFWKFRGNLANGAGATSLCEVYPLDFARTRLAADVGRRAQREFHLGGDCI IKIFKSDGLRGLYOGFNVSVOGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQS VTAVAGLLSYPFDTVRRRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSN VLRGWGGAFVLVYDEIKKYV" 341 a 304 c 357 g 318 t 102 bp upstream of NcoI site.	104. 997 /gene="ANTA" /note="ADPADT translocator protein" /codon_start=1 /protein_10="AAAAA1223.1" /db_xref="G1:339920" /db_xref="G1:339920"		Local		of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes Proc. Natl. Acad. Sci. U.S.A. 84 (21), 7580-7584 (1987)		Human lower leg muscle, cDNA to mkNA, (library of O clone pHMANT. Homo sapiens Fikarrota: Metazoa: Chordata: Cranjata: Vertebrata:	Human mitochondrial ADP/ J02966 J02966.1 GI:339919 J0P/ADT translocator.	1200 50 110005 17001 171111	841 ATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAAATATGTCTAA 894	781 GCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAGAGGC 840	721 TCCGGCCGAAAAGGGCCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAGATT 780 	661 GCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATGCAG 720 	
ORGANISM REFERENCE AUTHORS	RESULT 4 BC008664 LOCUS DEFINITION ACCESSION VERSION VERSION KEYMORDS	рь Оу Ор	ob oy	Qy Db	D Oy	Oy Db	Qy Db	Оy	Oy Db	Qу	Oy Db	Qy	Oy Db	Qy	Db
A Homo Suptens: A Homo Suptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1319) Strausberg,R.	88 8		721 TCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAGATT 780	661 GCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATGCAG 720		541 CAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGGATG 600 	481 ATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCTGTC 540	421 TTGCCTGCTGATGTGGCAGGCGCCCCCAGCGTGAGTTCCATGGTCTGGCGACTGTATC 480	GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG	301 GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCGTACTTTGCTGGTAACCTGGCGTCCGGT 360	241 TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA 300	181 ATCCCTAAGGAGCAGGCCTTCCTCCTTCTGGAGGGGTAACCTGGCCAACGTGATCCGT 240	121 GCCAGCAAACAGATCAGTGCTGAGAAGCAGTACAAAGGGATCATTGATTG	61 GTCTCCAAGACCGCGGTCGCCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 120	

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JOURNAL
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Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 13 Row: K Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502096
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk,
A.M., Holloway, M., Telford, B, Hodgson, A., Bd
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgppbs-r@mail.nih.gov
Tissue Procurement: ATCC
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   GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGT
                                                                                                               ATCCCTAAGGAGCAGGGCTTCCTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT 240
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NVLRGMGGAFVLVLYDEIKKYV"
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IKIFKSDGLRGLYQGFNVSVQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSNMIAQ
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/clone_lib="NIH_MGC_67"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus neonate male skeletal muscle cDNA to mRNA. Oryctolagus cuniculus
                                                                                                                                                                   Submitted (02-DEC-1997) Naohiro Yamaguchi, Osaka University, Division of Biophysical Engineering; Machikaneyama 1-3, Toyo Osaka 560, Japan (E-mail:n-yama@bpe.es.osaka-u.ac.jp, Tel:+81-6-850-6542, Fax:+81-6-850-6557)
                                                                                                                                                                                                                                                                                  skeletal muscle
J. Biochem. 335, 541-547 (1998)
2 (bases 1 to 932)
                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                         Identification of a 30kDa regulates calcium release
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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14. .910
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                                                                                           /organism="Oryctolagus
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/codon_start=1
                                                        /tissue_type="skeletal
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     932 bp
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                                                          muscle*
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                                                                                                                                                                                                                                                                  GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG
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GGCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAAATATGTCTAA
                                          ATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAGA
                                                                                     CAGTCTGGCCGGAAAGGGGCTGACATTATGTACACGGGGACAGTTGACTGCTGGAAGAAG
                                                                                                                                                 ACGGCAGTGGCCGGGCTGGTGTCCTACCCCTTTGACACTGTTCGTCGTAGGATGATGATG
                                                                                                                                                                ACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG
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/product="BAA33777.1"
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ISAEKQYKGIIDCVVRIPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKGIFLGG
VDRHKQFWRYFAGNLASGGAAGATSLCFYYPLDFAFTRLAADVEKGAAQREFSGLGNC
UTKIFKSDGLRGLYQGFNVSVQGIIIYRAAYFGYVDTAKGMLPDPKNVHIIVSMMIAQ
TVTAVAGLVSYPFDTVRRRMMNQSGRKGADIMYTGTVDCWKKIAKDEGAKAFFKGAWS
NVLRGMGGAFVLVLYDEIKKYY"
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Pred. No. 4.7e-159;
0; Mismatches 54;
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BOVING ADP/ATP translocase T1
M24102 J02845
M24102.1 GI:529414
ADP/ATP translocase; transloca
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1 (bases 1 to 1194)
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TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA
                                                                                                                                                                                                           ATCCCTAAGGAGCAGGCTTCCTCCTCCTCTGGAGGGGTAACCTTGGCCAACGTGATCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCATGGGTGGCGCTTTTGTATTGGTGTTGTATGATGAGGATCAAAAAATATGTCTAA
                                                                                                                                                                                   ATCCCCAAGGAGCAGGGCTTTCTCTCCTTCTGGAGGGGTAACCTGGCCAACGTGATCCGT
                                                                                                                                                                                                                                                                                 ATCTCCAAGACTGCTGTCGCGCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT
                                                                                             TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGATCTTCCTG
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/product="translocase"
/product="translocases"
/pr
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/db_xref="taxon:9913"
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Pred. No. 6e-154;
0; Mismatches 69;
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Oy Db	oy	Query Ma Best Loc Matches	BASE COUNT ORIGIN	FEATURES Source	TITLE JOURNAL	REFERENCE	VERSION KEYWORDS SCURCE ORGANISM	- I	RESULT 7	, 6 6	Db	Ϋ́ο	B 8	ďΩ	Oy C	D Oy	Db	Oy	οb	Oy	qa	î B	Оу
76 ATGGGGATCAGGCTTTGAGCTTCCTTAAGGACTTCCTGGCAGCGGCCATCGCCGCCCCCCCC	ATGGGTGATCACGCTTGGAGCTTCCTAAAGGACTTCCTGGCCGGGGCGGTCGCCGCTGCC 60	y Match Local Similarity 91.1%; Pred. No. 3.2e-151; hes 817; Conservative 0; Mismatches 77; Indels 3; Gaps 1;	/o: /dl /nc 295 a	Gene Logic, Inc. (US) Location/Qualifiers 11196	Elashoff,M.R. Molecular toxicology modeling L Patent: WO 0210453-A 1327 07-FEB-2002;	Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Rodentia; Sciurognat Rattus.		AX401651 1196 bp DNA linear PAT 06-JUN-2002 ON Sequence 1327 from Patent WOO210453. N AX401651		38 GCCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGAAAAATATGTCTAA [792 ATTGCAAAAGATGAAGGACCCAAGGCTTTCTTCAAAGGTGCCTGGTCCAACGTACTGAGA 851	ATTGCAAAAGAGGAGGCCAAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAGA	718 CACTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG 777	672 ACGCCGGTCGCGGGCTCGTGTCCTACCCCTTTGACACTGTCCGCCGTAGGATGATGATG 731	658 ACGGCAGTCGCAGGGCTGCTGCTCCTACCCCCTTTGACACTGTTCGTCGTAGAATGATGATGATG 717	ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCCTGGATGATTGCCCCAGAGTGTG	552 GTCCAGGCCATCATTATCTACCAGAGCCGCCTACTTTGGAGTCTATGATACGGCCAAGGGG 611	538 GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG 597	492 ATCACCAAGATCTTCAAGTCTGATGGCCTGAGGGGCCTCTACCAGGGTTTCAACCGTCTCG 551	478 ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT 537	421 TUNCTIONTENIO CAMBICO - COCCCAGCIGIAGTTCCATIGTCTGGGCGACTGT 477 111111 1 111111 1 1111111 11111 1111 1111 1111 432 CTGGCTGCCGACGGCAAGGGTGCCCGCCCCCAGCGGGACTTCACTGGTCTGGGCAACTGT 491	72 GGGGCAGCTGGGGCCACCTCCCTCTGCTTTGTCTACCCGCTGGACTTCGCTAGGACCAGG	
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) h,M., Yamaz cterizatior ondrial ade	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	adenine nucleotide translocator; isoform; mitochondrial inner membrane protein; solute carrier. Rattus norvegicus (strain:Sprague-Dawley) cDNA to mRNA. Rattus norvegicus	RATANTI 1196 bp mRNA linear ROD 28-APR-2000 Rattus norvegicus mRNA for mitochondrial adenine nucleotide translocator. D12770 D12770.1 GI:398592		838 GGCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAAATATGTCTAA 894	778 ATTGCAAAAGACGAAGGACCAAGGCCTTCTTCAAAAGGTGCCTGGTCCAATGTGCTGAGA 837 	718 CAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG 777 	658 ACGGCAGTCGCAGGGCTGCTGTCCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG 717	598 ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCAGAGTGTG 657	GTGCAGGGCATCATCATCACAGAGCTGCCTACTTCGGAGTCTATGACACTGCCAAGGGG	538 GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG 597	CTCACCAAGATCTTCAAGTCTGATGGCCTGAAGGGTCTCTACCAGGGTTTCAGTGTCTCT	496 CTGGCTGCCGACGTGGGCAAAGGGATCTTCCCAGCGTGAGTTCAATGGCTTGGGTGACTGT 555	421 TTGGCTGCTGATGTGGGCAGGCGCGCCCAGCGTGAGTTCCATGGTCTGGGCGAGCTGT 477	361 GGGCCGCTGGGGCACCTCCCTTTGCTTGTTACCCGCTTGGACTTTGCTAGGACCAGG 420 11		301 GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGT 360		241 TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA 300		196 GCCAGCAAACAGATCAGTGCAGAGAAACAGTACAAAGGCATCATTGATTG	121 GCCAGCAAACAGATCAGTGCTGAGAAGCAGTACAAAGGGATCATTGATTG	136 GTCTCCAAGACCGCGGTCGCCCCGATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 195

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemical, immunological, enzymatic, and genetic approaches to studying the arrangement of the peptide chain of the ADP/ATP carrier in the mitochondrial membrane
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Direct Submission
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Faculty of Pharmaceutical Sciences
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/protein_id="BAA02237.1"
/protein_id="BAA02237.1"
/db_xref="Gi:398593"
/translation="MGDOALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLOVOHASKO
/translation="MGDOALSFLKDFLAGGIAAAVSKTAVAPIERVKLKOVOHASKO
ISAEKQYKGIIDCVVRIPKEGGFLSFWRGNLAWVIFPPTQALLMPAFKOKYKOIFLGG
VDRHKQFWRFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKGSSOREFNGLGDC
LTKIFKSDGLKGLYQGFSVSVQGIIIYBAAYFGVYDTAKGMLPDPKNVHIIVSMNIAQ
SVTAVAGLVSYPFDTVBRRMMMQSGRKGADIMYTGTVDCWRKIAKADEGRKAFFKGAWS
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IMAGE:4500784, mRNA,
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Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Strausberg,R. Eukaryota; Metazoa; Mammalia; Eutheria; (bases 1 to 1070) Chordata; Rodentia; Craniata; Vert Sciurognathi;

REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT REMARK Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
DNA Sequencing by: Baylor College of Medicine Human Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A. Web site: http://www.hgsc.bcm.tmc.edu/cdna, Contact: amg@bcm.tmc.edu Center code: BCM-HGSC Sequencing Center Contact: MGC help desk NIH-MGC Project URL: http://mgc.nci.nih.gov s × Hulyk, S.W., Hale, Martin, R.G., Muzn Muzny,

Clone distribution: MGC clone distribution information can þe

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This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
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IRAK Plate: 29 Row: f Column: 24
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NVLRGMGGAFVLVLYDEIKKYV"
1 260 c 319 g 248 t
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/translation="MGDQALSFLKDFLAGGIAVAVIR**
/translation="MGDQALSFLKDFLAG
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/clone_lib="NIH_MGC_94"
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/db_xref="taxon:10090"
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90.6%;
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Pred. No. 7.4
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                                                     CDS
                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC heip uss.

Contact: MGC heip uss.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genry

Center, Stanford University School of Medicine, Stanford, CA

Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: Schmutz, J., Grimwood, J., Rodriquez, A., and Mi
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This clone was selected for full length sequencing passed the following selection criteria: Hexamer franchists, GenomeScan gene prediction.
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Submitted (28-FEB-2001) National Institutes of Health,
Gene Collection (MCC), Cancer Genomics Office, National
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(bases 1 to 1142)
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                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                 /clone="MGC:6027 IMAGE:3599576"
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                                                                          /note
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4, clone MGC:6027 ROD 07-AUG-2 (mitochondrial

07-AUG-2002

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                                                                                                                                                     ACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG
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                                  ATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAGA
                                                                                                                                       ACAGCGGTGGCGGGGCTGTCCTATCCGTTTGACACTGTTCGTCGTAGGATGATGATG
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/translation="MgdDALSFLkDFLAGGIAAAVSKTAVAP1ERVKLLLQVOHASKQ
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SVTAVAGLVSYPFDTVRRRMMOSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWS
NVLRGMGGAFVLVLYDEIKKYV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X74510
X74510.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
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TACTTCCCCACTCAAGCCCTGAACTTCGCCTTCAAAGACAAGTACAAGCAGATCTTCCTG
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/product="adenine nucleotide carrier"
/protein_id="CaA52616.1"
/protein_id="CaA52616.1"
/db_xref="c1:402628"
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/db_xref="SPTREMBL:062164"
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/clone_lib="lambda ZapII"
94. .990
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/clone="24"
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/db_xref="+-
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                                                               2 (bases 1 to 1273)
Ellison,J.W.
Direct Submission
Submitted (18-MAY-1995) Jay W
California, San Francisco, 3r
94143, USA
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U27315.1
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1 (bases 1 to 1273)
Ellison, J.W., Li, X., Francke, U. and
Rapid evolution of human pseudoautos
                                                                                                                                                                homologs
                                                                                                                                                                                                                      Eukaryota; Metazoa;
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                                                                                                                                                      Genome 7 (1),
 /organism="Mus musculus"
/strain="C57B1/6"
/db_xref="taxon:10090"
/chromosome="8"
                                                       Location/Qualifiers
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                                                                                                                                                                           pseudoautosomal
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                                                                          Ellison, Pediatrics, University and Parnassus, San Francisco, CA
                                                                                                                                                                                      Shapiro, L.J
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                                GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG
                                                                                                        ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT
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                    ATGCTGCCAGACCCCAAGAATGTGCACATTATCGTGAGCTGGATGATTGCGCAGAGTGTG
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1267. .1272
/gene="Ant1"
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ISAEKQYKGIIDCVVRIPKEQGFLSFWRGNLANVIRFPTOALMFAFKOKYKGIFLGG
VDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDLARTRLAADVGKGSSQFEFWGLGDC
LTKIFKSDGLKGLYQGFSVSVQGIIIYRAAYFGVYDTAKGMLPDPKNYHIIVSWMIAQ
SVTAVAGLVSYPFDTVRRRMMMQSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWS
NVLRGNGGAFVLVLYDEIKKYV"
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87. .983
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/product="adenine nucleotide translocase-1"
/protein_id="AAC52837.1"
/db_xref="G1:902008"
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1. .1273
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Sequence 3 from Patent W00132876.
XX134720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOKOR (US)
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                                                                GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGT
                                                                                                       ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC
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                                                     GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCCAACCTGGCCTCCGGC
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                                                                                                                                                                                                                                                                                MITOKOR (US)
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; M
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ATGGGTGATCACGCTTGGAGCTTCCTAAAGGACTTCCTGGCCGGGGCGGTCGCCGCTGCC
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                                        ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC
                                                   GTCTCCAAGACCGCGGTCGCCCCCATCGAAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 120
                                                                                            ATGACGGAACAGGCCATCTCCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC
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/db_xref="taxon:9606"
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                                                                                                                                                          63.18;
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                                                                                                                                              Score 564.2; DB 6;
Pred. No. 5.7e-110;
0; Mismatches 198;
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BC031912
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                                                   Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                        BC031912 1399 bp mRNA Homo sapiens, solute carrier family 25 (m adenine nucleotide translocator), member
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1399)
                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                       BC031912
                                                                                                                                                                                                                                                                                                           MAGE:5141625,
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Primates;
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Series: IRAK Plate: 42 Row: p Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM-HGSC
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GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG
                                                       GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGT
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laadkoykgivgcivripkeggylsfwrgklanvirpptqalbrafkoxykgiflgg
VDKHTOFWRYFAGNLASGGAAGATSLCFVYPDLDFARTRLAADVGKSGTEREFRGLEG
LVKITKSDGIRGLYQGFSVSVQGIIIVRAAYFGVYDTAKGMLPDPKNTHIVVSWHIAQ
TVTAVAGVVSYPFDTYRRRMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Cervix, carcinoma"
/clone_lib="NIH_MGC_12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"solute
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de translocator), member 6"
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Oy	421	TTGGCTGCTGATGTGGGCAGGCGCCCCCAGCGTGAGTTCCATGGTCTGGGCGACTGT 477
ОЬ	458	CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGGAGGTTCCGAGGCCTGGGAGACTGC 517
Oy	478	ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTTCAACGTCTCT 537
Đ,	518	CTGGTGAAGATCACCAAGTCCGGGGGGTCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 577
γO	538	GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG 597
В	578	GTGCAGGGCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC 637
9	598	ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCCAGAGTGTG 657
Db	638	ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG 697
97	658	ACGGCAGTCGCAGGGCTGGTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG 717
Dib	698	ACGGCCGTGGCCGGCGTGTCCTACCCCTTCGACACGGTGCGGCGGCGGCGATGATGATG
97	718	CAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG 777
Dib	758	CAGTCCGGGCCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 817
Οy	778	
Dio	818	ATCTTCAGAGATGAGGGGGCAAGGCCTTCTTCAAGGGTGCGTGC
0,7	838	
Оb	878	GGCATGGGGGGCCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 934

Search completed: June 22, 2003, 03:50:2 Job time : 1660 secs

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Result
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                           894
757.8
746.6
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                                                                                                                                                                                                                                     Score
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1: /SIDS2/gcgdata/g.
2: /SIDS2/gcgdata/g.
3: /SIDS2/gcgdata/g.
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ALIGNMENTS

RESULT 1
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ID AAD0 AAD00519; AAD00519 standard; cDNA; 894 BP Human adenine nucleotide translocator ANT1 cDNA. 29-AUG-2000 (first entry)

Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsopian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzhelmer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome; ss.

Homo sapiens.

11-MAY-2000 CDS WO200026370-A2 Location/Qualifiers
1..894 /*tag= a /product= "ANT1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, inherer's heraditary ontic neuropathy. schizophrenia, mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                   Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MEDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is a CDNA encoding adenine nucleotide translocator ANT1 from human brain.
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08-SEP-1999;
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TTGGCTGCTGATGTGGGCAGGCGCGCCCCAGCGTGAGTTCCATGGTCTGGGCGACTGTATC
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                                GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a method to produce adenine nucleotide translocator
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RESULT 2
AAS05901
ID AASC
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                                             Murphy AN,
Velicelebi
                                                                                                                          03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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                                                                                                                                                                                      10-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           adenine nucleotide translocator-1 (ANT-1)
                                                                                                                                                                                                                                                                                                                                                                                                            adenine nucleotide translocator-1; ANT-1;
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                                            Clevenger W,
G, Davis RE;
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New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.

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Matches 894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 894
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CTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCCAGAGTGTGACG
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Pred. No. 2e-
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                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial
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The invention relates to a recombinant expression construct (1) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (1) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (1) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating and in the polypeptide. Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -Example 1; Fig 1; 147pp; English.

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                                                                                                                                                                                  CTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCAGAGTGTGACG
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11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                    Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                   differential expression;
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                                                                                                                                                                                                                                                                                                                                                                                                      Rat sequence differentially expressed in response to a hepatotoxin
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19-JUN-2001;
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2001US-29023P.

2001US-290645P.

2001US-292336P.

2001US-295798P.

2001US-29745P.

2001US-298884P.

2001US-303459P.
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                                                                                                                                                                                                                                                 Johnson KR,
                                                                                                                                                                                                                                                Castle AL,
                                                                                                                                                                                                                                                 Elashoff MR;
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Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells

WPI;

2002-241625/29

Claim 1; Seq ID No 1327; 239pp; English.

Compounds or the progression of these toxic effects by determining the Compounds or the progression in tissues or cells exposed to the Coxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic ceffect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of cexpression in a tissue or cell sample exposed to the Pompound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that compount modulates the compount in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, a computer can a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification.

CC tanges in gene expression and for identifying toxicity markers in global changes in gene expression and for identifying toxicity markers in the probes compound or apent. Hepatotoxic the production or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxic agene which is differentially expressed in response to a hepatotoxic agent. The invention relates to methods for predicting toxic effects 0

RESULT 4 ABX63420

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RESULT 5
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91.1%;
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Pred. No. 5.1
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90.3%;
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                                                                                                                                                                                                                                                                                                                     Score 746.6;
Pred. No. 1e
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DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease: se
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Location/Qualifiers "Antl protein"

Wallace

Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or

English.

The present sequence is a mouse Antl degenerate cDNA sequence, cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ANT1.

Sequence 1259 BP; 274 A; 311 C; 339 G; 269 T; 66 other;

.6; DB 19; 1e-205;

ATCCCTAAGGAGCAGGCTTCCTCTCCTCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT GTCTCCAAGACGGCGGTCGCCCCGATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 0; Mismatches Caps 429 240 369 309 120 249

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RESULT 6
AAV36479
ID AAV3
XX
AC AAV3
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                                                                                                                                            Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease; ss.
            14-MAY-1998
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The presence sequence is the mouse Antl cDNA, cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ANT1.
                                                                                                                                                                                                                                                                                                                                                      Mice lacking heart-muscle adenine nucleotide translocator protouseful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions gene therapies
Sequence 1177
                                                                                                                                                                                                                                                                                                               Disclosure; Page 37-38; 61pp; English
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  282 A; 282 C; 326 G; 286 T; 1 other;
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TTGGCTGCTGATGTGGGCAGGCG---CGCCCAGCGTGAGTTCCATGGTCTGGGCGACTGT
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Query Match Best Local S Matches 809

Similarity

83.3%;

Score 745; 1 Pred. No. 2.9e 0; Mismatches

DB 19; 2.9e-205; 85;

Length 1177; Indels

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Gaps

; 608

Conservative

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                                                                                                                                                                                                                                                                                                                                                                             Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP, adenosine di-phosphate; adenosine tri-phosphate; appotosis; MPT; cann mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neurolepi antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neurolepi antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystodiabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and defines; hyperproliferative disorder;
                                       WPI; 2000-365619/31
P-PSDB; AAY71033.
                                                                                                                                                  03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                       myoclonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD00521 standard;
Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeuti
                                                                                  Ghosh
                                                                                             Anderson
                                                                                                                       (MITO-) MITOKOR.
                                                                                                                                                                                           03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenine nucleotide translocator ANT3 cDNA.
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against mitochondrial disease

Example 1; Page 166; 175pp; English

di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is a cDNA encoding admining nucleonide transference area from the present sequence. (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component inner mitochondrial membrane. It mediates transport of adenosine patent discloses a method to produce adenine nucleotide translocator adenine nucleotide translocator ANT3 from human brain. ō,

Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other;

Query Match Best Local 9 Matches 696;

Similarity

63.1%; 77.6%;

Conservative

0,

Score 564.2; DB 21 Pred. No. 5.5e-153; 0; Mismatches 198;

DB 21; 5e-153;

Indels

<u>س</u>

Gaps

Q Ş 망 Ş В Ş В δÔ Q 밁 Ş Db Ó В Qy B Ş 밁 Ş B 밁 밁 301 601 541 538 481 421 421 361 361 301 241 241 181 181 121 121 61 61 GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG TTGGCTGCTGATGTGGGCAGG----CGCGCCCAGCGTGAGTTCCATGGTCTGGGCGACTGT ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCAGAGTGTG GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA ATCCCTAAGGAGCAGGGCTTCCTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC ATGACGGAACAGGCCATCTCCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC 660 657 597 540 480 477 420 360 300 240 60 60 420 360 300 240 180

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ACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG

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     (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder;
                                                                                                                                                                   New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
                                                                                                                                                                                                                          WPI; 2001-291054/30
P-PSDB; AAU01200.
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 transition and/or alter the
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G, Davis F
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components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention of treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, parkinson's disease, Huntington's disease, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
GGCATGGGCGGGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAAAATATGTCTAA 894
                                                                                                                                                                                                                                                                            ACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG
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RESULT 9
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                                                                                                                                                      The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nucleic acid conding an adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC matrix for ADP in the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide. CC useful for determining the presence of an ANT polypeptide. CC useful for identifying an agent that binds to an ANT polypeptide. CC ANT from a biological sample, where the ANT ligand is covalently or non-CC covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the coding sequence of human ANT3.
                                                                                                        Query Match
Best Local
                                                                                           Matches
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                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-055598/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant expression construct locator polypeptides, comprises a ic acid encoding the polypeptide
 61
 GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 120
                                            ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC
                                                                                         Conservative
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                                                                                                                                                     BP; 174 A; 274 C; 287 G; 162 T; 0 other;
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1..897
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                                                                                                      63.18;
77.68;
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                                                                                                        Score 564.2; DB 24 Pred. No. 5.5e-153;
                                                                                         Mismatches 198;
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Human: nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                         chemokinetic; thrombolytic;
            leukaemia;
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Matches 695
                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, ActivinyInhibin activity, chemotactic/chemokinetic activity, heemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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25-APR-2000;
09-JUL-2000;
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Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
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03-AUG-2000;
                                                                                                                                                                                                                                                                  Sequence
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Wang Z,
Zhou P,
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                                                                                                                               ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGCTCAAGCTGCTGCAGCTCCAGCAC
                                                                                                                                                                                        ATGGGTGATCACGCTTGGAGCTTTCCTAAAAGGACTTCCTGGCCGGGCGGCTCGCCTCCC
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                   TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA 300
                                       GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
                                                                                                  GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 120
TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
                                                                                                                                                                            ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1000; 10078pp;
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T, Xu
Goodrich R,
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Pred. No. 1.8e-152;
D; Mismatches 199;
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AAI60583; AAI60583 standard; CDNA; 2035 ВР

Human polynucleotide

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22-OCT-2001

(first entry)

RESULT 11
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XX 22-OCT
XX Human
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OS Homo S
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PR 03-JUL
PR 04-JUL
PR 04-JUL 21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000; 14-SEP-2000; Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; leukaemia; ss. WO200153312-A1 26-DEC-2000; 26-JUL-2001 sapiens 2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000US-0653450. 2000US-0662191. 2000WO-US34263 thrombolytic; drug inflammation

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Matches 695
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P-PSDB; AAM41427.
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29-NOV-2000;
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ote: The sequence data for this patent did
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Zhou P,
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  ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGCTCTACCAGGGTTTCAACGTCTCT
                                                                                     GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTCGCCAGAACCCGC
                            CTGGCAGCGGACGTGGGAAAGTCAGGCACACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
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2000US-0727344
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Wehrman T,
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ku C, Xue AJ,
Drmanac RT;
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Ghosh SS;
             WPI; 2000-365619/31
P-PSDB; AAY71032.
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08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                     diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
Alzheimer's disease; Parkinson's disease; Huntington's disease; dyst
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di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MELAS), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is a cDNA encoding adenine nucleotide translocator ANT2 from human brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTGCCCCAGAGTGTG
                                                                                                                            GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGGTCTATGATACTGCCAAGGGG
                                                                                                                                                                                                                                                                                                                CTAGCAGCTGATGTGGGTAAAGCTGGAGCTGAAAGGGAATTCCGAGGCCTCGGTGACTGC
                                                                                                                                                                                                                                                                                                                                                                 TTGGCTGCTGATGTGGGCCA----GGCGCGCCCCAGCGTGAGTTCCATGGTCTGGGCGACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG
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ATGCTTCCGGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATCGCACAGACTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 9.6e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 G;
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The present sequence encodes for human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; adenine nucleotide translocator-2; ANT-2;
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                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 186pp;
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GGCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAAATATGTCTAA
                                                          ATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAAGA
                                                                                                                   CAGTCAGGGCGCAAAGGAACTGACATCATGTACACAGGCACGCTTGACTGCTGGCGGAAG
                                                                                                                                                              CAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG
                                                                                                                                                                                                                              ACGGCAGTCGCAGGGCTGCTGTCCTACCCCCTTTGACACTGTTCGTCGTAGAATGATGATG
                                                                                                                                                                                                                                                                                      ATGCTTCCGGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATCGCACAGACTGTC
                                                                                                                                                                                                                                                                                                            ATGCTGCCTGACCCCAAGAACGTGCACATTTTTTGTGAGCTGGATGATTGCCCCAGAGTGTG
                                                                                                                                                                                                                                                                                                                                                                       GTGCAGGGTATTATCATCTACCGAGCCGCCTACTTCGGTATCTATGACACTGCAAAGGGA
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                                                                                                                                                                                                        ACTGCTGTTGCCGGGTTGACTTCCTATCCATTTGACACCGTTCGCCGCCGCATGATGATG
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Pred. No.
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1.6e-150;
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RESULT 14
AAS16689
ID AAS1
                                                               Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS16689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS16689 standard;
                                                                                                                                      WPI; 2002-055598/07.
P-PSDB; AAU10379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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The invention relates to a recombinant expression construct (I)
                               Example 1; Fig 1; 147pp; English.
                                                                                                                                                                                                                                                                                     11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                        11-MAY-2001; 2001WO-US15416
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                                                                                                                                                                                                                                                 (MITO·) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenine nucleotide translocator;
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                                                                                                                                                                                                               Davis
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Adenine nucleotide translocator 2 (ANT2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
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Pei
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                                                                                                                                                                                              Clevenger W,
Y, Carroll !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide translocator
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                                                                                                                                                                                                                   Szabo
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CC comprising a regulated promoter operably linked to a nucleic acid CC comprising an adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ant polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide CC of interest to a mitrochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. (C expressed as a fusion protein with the polypeptide of interest. (C expressed as a fusion protein with the polypeptide of interest.) (C expressed as a fusion protein with the polypeptide of interest.) (C expressed as a fusion protein with the polypeptide of interest.) (C expressed as a fusion protein with the polypeptide of interest.) (C expressed as a fusion protein with the polypeptide.) (C expressed as a fusion protein with the polypeptide.) (C expressed as a fusion protein with an ANT polypeptide.) (C expressed as a fusion agent that binds to an ANT polypeptide.) (C expressed as a solid phase. Detectably labeled ANT ligand is also cuseful for identifying an agent that interacts with an ANT polypeptide.) (C The present sequence represents the coding sequence of human ANT2.)

897 ВP; 209 A; 223 C; 246 G; 219 T; 0 other;

61.98; 76.88;

Length

Query Match

Ş 멍 Best Loc Matches 1 Similarity 689; Conserv Conservative 0; Score 553; DB Pred. No. 9.6e 0; Mismatches DB 24; 9.6e-150; hes 205; <u>ω</u> Gaps 60

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ATGACAGATGCCGCATTGTCCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCCGCAGCC 60

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RESULT 15
AAS91243
ID AAS9
XX AAS9
AC AAS'
AC AAS'
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            Homo sapiens
                                Human; chromosome mapping; gene mapping;
food supplement; medical imaging; diagnos
                                                                                                                                AAS91243 standard;
                                                                DNA encoding novel human diagnostic protein #27047.
                                                                                      13-FEB-2002
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                                                                                                                                                                                  ATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAGA
                                                                                                                                                                                                                                                                       CAGTCAGGGGGCAAAGGAACTGACATCATGTACACAGGCACGCTTGACTGCTGGCGGAAG
                                                                                                                                                                                                                                                                                   CAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG
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                                                                                     (first entry)
                                                                                                                                CDNA;
                              apping; gene therapy; forensic;
diagnostic; genetic disorder; ss
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The invention relates to isolated polynucleotide (1) and (1) polypeptide (II) sequences. (1) is useful as hybridisation probes, (2) polymerase chain reaction (PCR) primers, oligomers, and for chromosome (2) and gene mapping, and in recombinant production of (II). The (II) gene mapping, and in recombinant production of (II) from the printed (II) are tassed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a noolecular weight markers and as a noolecular weight markers and as a molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating (III) are useful for the printed (III) are useful for the printed (III) are useful for the printed (III) are treating (III) are useful for the printed (III) are treating (III) are treating (IIII) are treating (III) 
     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No
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23-AUG-2000;
Sequençe 1156
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                                                      ftp.wipo.int/pub/published_pct_sequences.
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2000US-0649167
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264 A; 286 C; 302
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                                                TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA
                                                                                                   ATCCCTAAGGAGCAGGGCTTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT
                                                                                                                                                 TACTTCCCCACCCAGGCTCTTAACTTCGCCTTCAAAGATAAATACAAGCAGATCTTCCTG
                                                                                     ATTCCCAAGGAGCAGGGAGTTCTGTCCTTCTGGCGGGGTAACCTGGCCAATGTCATCAGA
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Ouery Match Best Local S Matches

691;

Conservative

Similarity

58.5%; 76.8%;

Score 523.2; Pred. No. 4.5e

O; Mismatches

No. 4.5e-141;

203;

indels Length

6;

Gaps

253		500	7
894		836	οy
892	ATTGCTCCGTGATGAAGGAGGCAAAGCTTTTTTCAAGGGTGCATGGTCCAATGTTCCTCA	833	Ъ
835	ATTGC - AAAAGACGAAGGAGCCAAGGCCCTTCTTCAAAGGTGCCTGGTCCAATG - TGCTGA	778	Ŷ
832		//3	OD
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777	CAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG	718	Ŷ
772	ACTGCTGTTGCCGGGTTGACTTCCTATCCATTTGACACTGTTCGCCGCCGCATGATGATG	713	DЬ
717	ACCGCAGTCCCCAGGGCTGCCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGATG	859	Οy
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712		653	В
657	ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCCTGGATGATTGCCCCAGAGTGTG	. 598	οy
652	GTGCAGGGTATTATCATCTACCGAGCCGCCTACTTCGGTATCTATGACACTGCAAAGGGA	593	Βħ
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597	GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG ;	538	Ş
592	CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCT	533	ρţ
537		478	Š
532	CTACCAGCTGATGTGGGTAAAGCTGGAGCTGAAAGGGAATTCCGAGGCCTCGGTGACTGC	473	Βb
477	TTGGCTGCTGATGTGGGCAGGCGCGCCAGCGTGAGTTCCATGGTCTGGGCGACTGT	421	ô
472	GGTGCCGCAGGGGCCACATCCCTGTGTTTTGTGTACCCTCTTGATTTTGCCCGGTACCCGT	413	Вb
420		361	ý,
412	353 GGTGGTGTGGACAAGAGAACCCCAGTTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGGT 412	353	Dlo

Search completed: June 22, 2003, 03:22:31 Job time: 196 secs

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Result
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-961-871-9
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US-09-103-840A-1 US-09-103-840A-2 US-09-103-840A-1 US-09-103-840A-1 US-09-234-613-61 US-09-234-613-61 US-09-153-804-4 US-09-153-804-4 US-09-568-409-1 US-09-568-486-1 US-09-568-486-1 US-09-568-486-1 US-09-568-485-1 US-09-443-501A-2 US-08-246-485-1 US-08-246-485-1 US-08-246-485-1 US-08-246-485-1 US-08-246-485-1

ALIGNMENTS

; Sequence 11, Applicat ; Patent No. 6013858 ; GENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 78-96 TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080 TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1259 base pairs PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/ FILING DATE: 01-NOV-1996 ATTORNEY/AGENT INFORMATION: NAME: Ferber, Donna M. REGISTRATION NUMBER: 33,87 APPLICANT: Wallace, Douglas C. APPLICANT: Graham, Brett H. APPLICANT: MacGregor, Grant R. APPLICANT: MacGregor, Grant R. TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine TITLE OF INVENTION: Nucleotide Translocator Protein and NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: double TODOLOGY: not relevant COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk FEATURE: NAME/KEY: TOPOLOGY: no MOLECULE TYPE: HYPOTHETICAL: NO STREET: 5370 M CITY: Boulder STATE: Colorad APPLICATION NUMBER: US/08/961,871 FILING DATE: 31-OCT-1997 CLASSIFICATION: 800 COUNTRY: ADDRESSEE: LOCATION: 1, Application US/08961871 6013858 Colorado E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201 SU DNA (genomic) us 60/030,017 33,878 and Methods

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RESULT 2
US-08-961-871-9
Sequence 9, Ap
Patent No. 601
GENERAL INFOR
APPLICANT:
APPLICANT:
Sequence 9, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
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APPLICATION NUMBER: US 60/030,
FILING DATE: 01-NOV-1996
ATTONNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMUNICATION: NUMBER: 78-9
TELECOMMUNICATION: 09-8080
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8089
INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 Dase pairs
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Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1177 base TYPE: nucleic acid STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 745; DB
Pred. No. 1.4e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                            TELEFAX: (212) 869-9741/88
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                      OPERALING SOFTWARE: PatentIn Release #1.0, ...
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US_08/518,878B
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: F10PDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT
                    SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
                                                                                                                        REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: N
                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01
FILING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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Coruzzi, Laura A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                        (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1
                                                                                                                                                                         7853-036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/08294522B Patent No. 5741666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
  INFORMATION FOR
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 48
                                     TELEPHONE: (212) 790-9090
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Aven
CITY: New York
STATE: New York
ZIP: 1036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                  APPLICATION NUMBER: US/08/294,522B FILING DATE: 23-AUG-1994 CLASSIFICATION: 514
                                                                                REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              E: Pennie & Edmonds
1155 Avenue of the Americas
:: (212) 790-9090
(212) 869-8864/9741
OR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                         Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Tartag
CLASSIFICATION.
ATTORNEY/AGENT INFORMATION:
NAME: CCTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7853-0031-999
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositio
TITLE OF INVENTION: Treatment
                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                     APPLICATION NUMBER: US/08/470,868A FILING DATE: 06-JUN-1995 CLASSIFICATION: 530
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
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Local Similarity 44.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTTCGTCGTAGAATGATGCAGTCCGGCCGGAAAGGGGCCCGATATTATGTACACGG 754
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                                                                                                                                                                                                                                                                                                                                            1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions and Methods for the Treatment of Body Weight Disorders, Including Obesity
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US-08-807-861A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application US/08807861A Patent No. 5853975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TITLE OF INVENTION: REGULATION OF BODY WARRANT THE NUMBER OF 
                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Aven
CITY: New York
STATE: New York
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APPLICATION NUMBER: FILING DATE: 26-FE
                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                             RY: U.S.A.
10036-2711
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93; Conservative
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(212) 869-8864
                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pennie & Edmonds LLP
        26-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%;
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                                        US/08/807,861A
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                                                                                                                        Version #1.30
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Best Local S
Matches 193
                                                                                Sequence 38, Applicat Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartag
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TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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               APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORD
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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STRANDEDNESS: single
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 Pennie & Edmonds LLP
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06-JUN-1995
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23-AUG-1994
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                                               BODY WEIGHT DISORDERS, INCLUDING OBESITY
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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NAME: Coruzzi, Laura A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: N
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REGISTRATION NUMBER:
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TRY: U.S.A.
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                                        GGACCTCTCCCAATGTTGCTCGTAATGCCATTGTCAACTGTGCTGAGCTGGTGACCTATG
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(212) 869-9741/8864
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26-FEB-1997
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US-08-946-719A-38
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Matches 193; Conserv
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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TOPOLOGY: line
MOLECULE TYPE: [
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
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TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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FILING DATE: 8-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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GCTGGATGATTGCCCAGAGTGTGACGGCAGTCGCAGGGCTGCTCCTACCCCCTTTGACA 694
                                               GCCTGTATGATTCTGTCAAACAGTTCTACACCAAGGGCTCTGAGCATGCCAGCATTGGGA
                                                                              GAGTCTATGATACTGCCAAGGGGGATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGA 634
                                                                                                               TCTACAATGGGCTGGTTGCCGGCCTGCAGCGCCAAATGAGCTTTGCCTCTGTCCGCATCG
                                                                                                                                                                              AGTACCGCGGTGTGATGGGCACCATTCTGACCATGGTGCGTACTGAGGGCCCCCGAAGCC 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tartaglia, Louis A.
JENTION: COMPOSITIONS FOR THE TREATMENT AND
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                                                                                                                                                                                                                                               Score 46.6; DB 3;
Pred. No. 0.00074;
0; Mismatches 244;
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                                                                                                                                                                                                                                               244;
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US-08-642-255-60
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             PATENT NO. 5773249

GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular WOTTLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                   Sequence 60, App....
Some No. 5773249
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/142,565A CURRENT FILING DATE: 1999-06-30 EARLIER APPLICATION NUMBER: 9704551.2 EARLIER FILING DATE: 1997-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 97305305.1 EARLIER FILING DATE: 1997-07-16 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1192
TYPE: DNA
ORGANISM: HOMO SAPIEN
                                                                                                                                                                                                                835 AGAGGCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAA 884
                                                                                                                                                                                                                                                                                                                                                                                                    640 ATACACCTCGGGCCATCCAGGAGCGACAGAAATACAGCGGGACTATGGACGCCTACAGA
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                                                                                                                                                                                                                                                                                                                                       775 AAGATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTG 834
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Similarity 52.9%;
                                                                                                                                                      AGGAATGCTATCGTCAACTGTGCTGAGGTGGTGACCTACGACATCCTCAA 809
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Application US/08642255
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pred. No. 0.014; 
0; Mismatches 80; Indels
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High Molecular Weight Collagen-Like

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TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 66
                                                                                                                                                                                                                                      GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: JBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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DESCRIPTION:
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LENGTH: 810 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: A55556-3/BIR TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                          APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                     APPLICANT:
                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCATGCCAGCAAACAGATCAGTGCTG 142
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                                                                                                                                                                                                                                                                                                                                                                                             TCTCCTTC 210
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            E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
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                                                                                                                                                 Au-Young, Janice
                                                                                                                                                                     Shah, Purvi
                                                                                                                                                                                 Hillman, Jennifer L.
Bandman, Olga
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Pred. No. 0
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US-09-234-613-68
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                        Sequence 68, Application US/09234613 Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pair
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
                                                                                                                                 APPLICANT:
                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                            CORRESPONDENCE ADDRESS
                                              APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: SYNOOATO1
CLONE: 724157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                             670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 TTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGACCCTC
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Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                 Shah, Purvi
Au-Young, Janice
                                                                                                                                                                   Hillman, Jennifer L.
Bandman, Olga
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Gaps

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RESULT 13
US-09-188-930-23
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; Fatent No. 6150502
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LIBRARY: SYNOO.

CLONE: 724157
US-09-234-613-68
                                                                                                                                                                                       GENERAL INFORMATION:
                    APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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                NUMBER OF
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APPLICATION NUMBER: US/08
FILING DATE: September 2:
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Disket
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/234,613 FILING DATE:
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ZIP: 94304
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Similarity 48.4%;
                SEQ ID NOS: 348
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FastSEQ for Windows Version 3.0
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ber 23, 1997
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Sequence 5, Application US/08937466
Patent No. 5846779
GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-262
                                                                                                                                                                 RESULT 15
US-08-937-466-5
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LENGTH: 997
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Best Local Similarity 55.9%;
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Best Local Similarity 55.9
Matches 71; Conservative
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APPLICANT: Murison, James Greq
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
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ORGANISM: mouse
                                                                                                                                                                                                                                                                                          130 CAGATCA 136
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                                                                                                                                                                                                                                                   725 AACAACA 731
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o. 6150502
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Pred. No. 0.34;
0; Mismatches 56;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIO Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
NOLECULE TYPE: cDNA
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Search completed: June 22, 2003, 02:39:02 Job time: 57 secs
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
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ZIP: 94010
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                                                                          682 GAACTGGAGGAGAGAGAATACAGAGGGACTATGGATGCCTACAGAACCATCGCCAGGG
                                                                                                                                                                                                                                                             728 GGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAGATTGCAAAAG 787
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Minimum
Maximum
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Perfect score:
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length: 2000000000
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Match Length DB
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                     100.0
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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:/cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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9 US-09-185-904A-2

10 US-09-811-094-2

10 US-09-810-644-2

11 US-10-044-090-152

12 US-10-171-581-48

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Sequence 1, Appli
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Sequence 2096, Ap
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23.7	23.8	23.9	24.0	24.0	24.8	25.8	26.0	26.4	26.5	26.7	27.0	27.1	30.1	30.4	30.5	30.5	30.5	30.8	32.4	33.8	35.4	36.4	41.2	43.0	43.2
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US-09-734-569-169	US-09-801-368-251	US-09-960-352-10948	US-09-864-761-1488	US-09-770-445-7	US-09-918-995-5524	US-09-918-995-8792	US-09-960-352-14289	US-09-834-975-995	US-09-918-995-16539	US-09-960-352-12424	US-09-864-761-1408	US-09-918-995-4700	US-09-918-995-37948	US-09-918-995-26014	US-09-960-352-10722	US-09-918-995-1495	US-10-198-846-6781	us-09-918-995-9153	US-09-833-790-161	US-09-918-995-3573	US-09-918-995-3627	US-09-918-995-3021	US-09-910-943-105	US-09-918-995-6148	US-09-918-995-6070
Sequence 169, App	Sequence 251, App	Sequence 10948, A	Sequence 1488, Ap	Sequence 7, Appli	Sequence 5524, Ap	Seguence 8792, Ap	Sequence 14289, A	Sequence 995, App	Sequence 16539, A	Sequence 12424, A	Sequence 1408, Ap	Sequence 4700, Ap	Sequence 37948, A	Sequence 26014, A	Sequence 10722, A	Sequence 1495, Ap	Sequence 6781, Ap .	Sequence 9153, Ap	Sequence 161, App	Sequence 3573, Ap	Sequence 3627, Ap	Sequence 3021, Ap	Sequence 105, App	Sequence 6148, Ap	Sequence 6070, Ap

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/185,904A
COURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 894
TYPE: DNA
ORGANISM: Homo sapien
US-09-185-904A-1
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                                                                                                                                                                                     Matches 894; Conservative
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: THANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING
TITLE OF INVENTION: THEREFOR
TITLE REFERENCE: 660088 420
                                                                                                                                                                                                     Local Similarity
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                                                          61 GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT
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Pred. No. 4.8e-287;
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUTTITLE OF INVENTION: NOVEL ANT LIGANDS AND SETILE REFERENCE: 660088.420D4
CURRENT APPLICATION UNMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTMARE: FOSTSEQ FOR Windows Version 3.0
SEQ ID NO 1
LENGTH: 894
TYPE: DNA
                                                                                                                         GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiler, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Sounitra S.

APPLICANT: MOOS, Walter H.

APPLICANT: Pei, Yazhong
                                                                                                                                                                                                                                                    Sequence 1, Application US/09811094 Patent No. US20010044144A1
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; Sequence 1, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
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94; Conservative
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: LENGTH: 894
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US-09-810-644-1
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APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUC
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SC
FILE REFERENCE: 660088.42003
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
Schosh, Sounitra S.
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                                     ATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCTGTC
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Pred. No. 4.8e-287;
Mismatches 0;
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; NAME/KEY: misc_feature
; LOCATION: 1435, 1436, 1437, 1438,
; LOCATION: 1445, 1446, 1447, 1448,
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13437
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Sequence 13437, Application US/10198846

: Publication No. US20030099974A1

: GENERAL INFORMATION:
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Best Local S
Matches 889
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SOFTWARE: FastSEO for Windows Version
SEO ID NO 13437
LENGTH: 1711
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APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTLFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
"FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198,846
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1, 2, 1397, 1398, 1399, 14
LOCATION: 1406, 1407, 1408, 1409, 14
LOCATION: 1416, 1417, 1418, 1419, 14
LOCATION: 1426, 1427, 1428, 1429, 14
OTHER INFORMATION: n = A,T,C or G
FEATURE:
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              TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA
                                                                                              GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT
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Pred. No. 6.4e-280;
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APPLICANT: Mondrick, Donna
APPLICANT: Mondrick, Donna
APPLICANT: Johnson, Kory
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-16
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
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: Sequence 1327, Application US/09917800A

: Patent No. US20020119462A1
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PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1327
LENGTH: 1196
TYPE: DNA
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APPLICANT: S2.abo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEO ID NOS: 33
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ORGANISM: Homo
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                                                                                                ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT
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Wiley, Sandra Eileen
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Pred. No. 2.9e-177;
0; Mismatches 198;
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GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Soutt W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088, 42004
CURRENT FILING DATE: 2001-03-14
NUMBER OF SECTOR OF WILLIAM: Vacation 3 0
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LENGTH: 897
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                                                 TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA 300
                                                                                                ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC
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Pred. No. 2.9e-177;
0; Mismatches 198;
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-644-3
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Sequence 3, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
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              Query Match
Best Local Similarity
Matches 696; Conserv
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Soutt W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Hoos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088, 42003
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               Conservative
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APPLICANT: Tang, Y. Tom APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Asundi, Vinod APPLICANT: Zhang, Jie APPLICANT: Ren, Feiyan APPLICANT: Chen, Rui-hong APPLICANT: Zhao, Qing A.
                                                                               Sequence 687, Application No. US200 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: No. US20030104529Alel Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
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Wang, Jian-Rui
Zhou, Ping
              GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG 597
                                                                      ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT
                                                                                                             CTGGCAGCGGACGTGGGAAAGTCAGGCACACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
                                                                                                                         TTGGCTGCTGATGTGGGCAGG----CGCGCCCAGCGTGAGTTCCATGGTCTGGGCGACTGT
                                                                                                                                                                 GETGCGGCCGGCGGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTCGCCAGAACCCGC
                                                                                                                                                                                 GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG
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GTGCAGGGCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
                                                       CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
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Pred. No. 1.1e-176;
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; TYPE: DNA
; ORGANISM: Homo sapien
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: SEQ ID NO 2

: LENGTH: 897
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APPLICANT: Davis, Robe
APPLICANT: Clevenger,
APPLICANT: Wiley, San
APPLICANT: Willer, Sca
APPLICANT: Scabo, Ton
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Best Local S
Matches 689
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                                                     TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA
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                                                                                 ATTCCCAAGGAGCAGGAAGTTCTGTCCTTCTGGCGCGGTAACCTGGCCAATGTCATCAGA
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Clevenger, William
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Sequence 2, Application US/09185904A Patent No. US20020177185A1
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                                                                                                                                                                                                                                                                                  APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Glosh, Soumitra S.
APPLICANT: Glosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS
TITLE OF TIVENTION: THEREFOR
FILE REFERENCE: 660088.420
                                                                                                                                                                                                  FastSEQ for Windows Version
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Score 553; DB 9; Length 897; Pred. No. 1.6e-173; N.
0; Mismatches 205; Indels
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; TYPE: DNA
; ORGANISM: Homo sapien
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
                                            Query Match
Best Local S
Matches 689
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US Patent No. US20010044144A1 GENERAL INFORMATION:
                                                                                                                                                APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.42004
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
                                                           Local Similarity
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
ATGGGTGATCACGCTTGGAGCTTCCTAAAGGACTTCCTGGCCGGGGCGGTCGCCGCTGCC
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                                              Conservative
                                                          61.9%;
76.8%;
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                                              0;
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Pred. No. 1.6e-173;
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; Sequence 2, Application US/09810644
; Patent No. US20020012992A1
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APPLICANT: Anderson, Christen M
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileer
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Yazhong
                                                                                                                                  GENERAL INFORMATION:
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Clevenger, William Wiley, Sandra Eileen Willer, Scott W. Szabo, Tomas R. Ghosh, Soumitra S. Moos, Walter H. Pei, Yazhong
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LENGTH: 897
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Best Local
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
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SOFTWARE: FastSEQ for
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ATTGCTCGTGATGAAGGAGGCAAAGCTTTTTTCAAGGGTGCATGGTCCAATGTTCTCAGA
                                                CAGTCAGGCGCAAAGGAACTGACATGATGTACACAGGCACGCTTGACTGCTGGCGGAAG
                                                             CAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG
                                                                                                  ACTGCTGTTGCCGGGTTGACTTCCTATCCATTTGACACCGTTCGCCGCCGCATGATGATG
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILLNG DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 152
LENGTH: 2592
                                                                                                                                                                              CCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGG
                                                           GTTACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                 GAATCCCTAAGGAGCAGGGCTTCCTCTCTCTGGAGGGGTAACCTGGCCAACGTGATCC
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: PUBLICATION INFORMÁTION:
DATABASE ACCESSION NUMBER: J03592
DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-48
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US-10-171-581-48
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APPLICANT: Linsley, Peter
APPLICANT: Mao Mao
TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
FILE REFERENCE: 9301-157-99
CURRENT APPLICATION NUMBER: US/10/171,581
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 366
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TYPE: DNA
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                         TTTGCCAGAACCCGCCTGGCAGCGGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA
                                                           TTTGCTAGGACCAGGTTGGCTGCTGATGTGGGCAGG---CGCGCCCAGCGTGAGTTCCAT 462
                                                                                                                                                                                                              AAGCAGCTCTTCTTAGGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCGCTACTTTGCTGGT 345
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77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 488; DB 9; Pred. No. 7.5e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1116;
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 658
SOFTWARR: PATENTIN VERSION 3.0
SEQ ID NO 213
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APPLICANT: Augustus, Meena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 213, Application US/09969708 Patent No. US20020102532A1
                                                                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                        LENGTH: 1116
TYPE: DNA
ORGANISM: Homo sapiens
     121
                                                                                                                                                                                                                          54.6%; al Similarity 77.8%; 616; Conservation
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GCCAACGTGATCCGTTACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTAC
                                                                       CTGCAGGTCCAGCACGCCAGCAAGCAGCAGCAGCCGCCGACAAGCAGTACAAGGGCATCGTG
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Pred. No. 7.5e-152;
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                       GATACTGCCAAGGGGATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATG
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                                                                                                        ATTGCCCAGAGTGTGACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGT 702
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AAGGTGATCTAA 789
      AAATATGTCTAA 894
                                                                         CGGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTC
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Search completed: June 22, 2003, 03:19:00 Job time : 130 secs

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Maximum Match 100%
Listing first 45 summaries
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   761.4
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1 atgggtgatcacgcttggag.....agatcaaaaaatatgtctaa 894
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Gapop 10.0 , Gapext 1.0
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BM230491 K0296B10-
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CI_CGAP_Skn 1:13905347 1:13905347 tazoa: Chorheria: Prim o 964) //mgc.nci.n itutes of H 1999 //mgt.nihement: Jame Preparatio Arrayed by Incyte Ge bution: MGC the I.M.A. 11019 592 row: d sequence st tion/Qualif	9990 13 8879 13 8882 13 9948 13 9948 13 9948 13 9866 12 13 13 13 13 13 13 13 13 13 13 13 13 13
3 Homo sapiens data: Craniata: ates; Catarrhir ih.gov/. ealth, Mammalia ealth, Mammalia: Cleaver, M.D. cleaver, M.D. i. Life Technol The I.M.A.G.E. nomics, Inc. clone distribu G.E. Consortium G.E. Consortium Column: 07 op: 835.	B1545249 B1408731 B14408731 B14508731 B14508731 B145087326 B1467026 B1677026 B1677026 B16755359 B1755550 B1755550 B16410853 B056581 B16408467 B16408467 B16408467 B16408467 B16408467 B16408467 B16408467 B16408467 B1640868 B1736370 B164088 B1736372 B164088 B1736372 B1660308 B1736372 B1660308 B1736372 B1603210 B1736372
cDNA clone IMAGE:4745430 5 Vertebrata: Euteleostomi; i; Hominidae; Homo. In Gene Collection (MGC) Consortium (LLNL) DNA Lion information can be CLLNL at:	B1545249 603187373 B1408731 602965692 B1458368 603198738 BM459526 AGENCOURT B141990 6029871499 B1256359 602975222 B0947818 AGENCOURT B1411906 603027226 B1545550 603027226 B1545551 603027226 B1666992 MCENCOURT B1610853 602963777 B0572174 U1 M-FB0-B1525539 60296374 B1410725 602966284 B1410725 602964284 B1410725 602964258 B1544547 603241881 B16438016 AGENCOURT B1088005 602852477 B1411055 602987310 B141676 602987310 B141676 602987310 B141676 602987310 B141676 602987310 B141676 602987310 B141676 60298737 B1598151 603168426 B0938203 AGENCOURT B1904612 603168426 B0938203 AGENCOURT B160568 603223209 B1732570 603256888 B1735372 603356857 B1603210 603249858

BASE ORIGI

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Matches Query Match Best Local

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 AGGCATGGGGGGTGCTTTTGTATTGGTGTTG
                                   GCAGTCCGCGCGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAG
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                                                                  GATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAG
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/db_xref="taxon:9606"
/clone="IMAGE:4745430"
/clone=LiMaGE:4745430"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: skin; vector: pCMV-SPORF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 249 C 310 g 217 t
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL556492
AL556492 LTI_NFL006_PL2
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Genoscope - Centre National de Sequencage
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Mammalia; Eutheria;
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                                 TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA
                                                                                                                   TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTTTTTA
                                                                                                                                                                    ATCCCTAAGGAGCAGGGCTTCCTCCTCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco Ry Sites of the primer 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
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/db_xref="taxon:9606"
/clone="CSODK006YA17"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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98.8%;
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Pred. No. 4.5e-196;
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                                                                                                                                                                                                                                                                                                   National institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, (Email: cdna@lgsun.grc.nia.nih.gov Plate: K0296 row: B column: 10 Seq.primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                       Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y.,
Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Contact: Dawood B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note-*Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2 NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.
                                                                                                                     /tissue_type="Unfertilized
                                                                                                                                          /clone_lib="NIA Mouse Unfertilized
)".
                                                                                                      /lab_host="DH10B"
                                                                                                                                                                 /clone="K0296B10"
                                                                                                                                                                               /db_xref="niaEST:K0296B10-3"
/db_xref="taxon:10090"
                                                                                                                                                                                                               /strain="C57BL,
                                                                                                                                                                                                                           /organism="Mus musculus"
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treated with 74 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sall and Notl enzymes and cloned into Sall/Notl site of psPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
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Score 733.2; DB 13; Pred. No. 3.1e-194; 0: Mismatches 87;

Length 1073;

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Gaps

GTTGGCTGCTGATGTGGGCAGGCG---CGCCCAGCGTGAGTTCCATGGTCTGGGCGACTG AATCCCTAAGGAGCAGGCCTTCCTCTCTCTGGAGGGGTAACCTGGCCAACGTGATCCG GTCTNCCAAGACGCGCTCGCNCCGATCGAGAGGGTCAAACTGCTGCTGCTGCAGGTCCAGCA GTCT-CCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCTGCAGGTCCAGCA ATGGGGGATCAGGCTTTGAGCTTTCTTAAGGACTTCCTGGCAGGTGGCATCGCCGCCGCC GACAGCGGTGGCGGGCTGGTGTCCTATCCGTTTGACACTGTTCGTCGTAGGACGATGAT GACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATGATGAT TCTCACCAAGATCTTCAAGTCGGACGGCCTGAAGGGTCTCTACCAGGGTTTCAGTGTCTC TATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGGCTCTACCAGGGTTTCAACGTCTC GCTGGCTGCCGACGTGGGCAAGGGATCTTCCCAGCGAGAATTCAATGGGCTGGGCGACTG TGGGGCAGCTGGGGCCACCTCCCTCTGCTTCGTCTACCCGCTGSACTTTGCTAGGACCAG TGGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAG GGGAGGCGTGGATCGCCATAAGCAGTTCTGGCGCCTACTTTGCTGGTAACCTGGCCTCTGG AGGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGG GTACTTCCCCACTCAAGCCCTGAACTTCGCCTTCAAAGACAAGTACAAGCAGATCTTCCT TTACTTCCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTT 240 300 656 596 360 420 536 480 476 540 419 600 660 720 239 780 840 119 359 900

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Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
             AGGCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGATCAAAAAATATGTCTAA 89-
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/db_xref="taxon:9606"
/clone="IMAGE:5196080"
/clone=1ib="NIHL_MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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                                                                                                                          BP 191
Email:
                                                                                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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AL561542 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0DL011YJ23 5
prime, mRNA sequence.
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                                          /organism="Homo sapiens"
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/tissue_type="B cells from Burkitt lymphoma
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                                                                                                        Location/Qualifiers
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Primates;
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BASE COUNT
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                                                              TGATGCAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAGTTGACTGCTGGA
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                                GGAAGATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAG 814
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http://fulllength.invitrogen.com"
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96.5%;
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Pred. No. 2.2e-189;
3; Mismatches 16;
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맑

Оу 36	Oy 30	Qy 24 Db 33	Qy 181 Db 271	Оу 121 Db 211	Оу б рь 15	Oy Db	Query Match Best Local Si Matches 744;	RESULT 6 BM466452 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT BASE COUNT ORIGIN
)1 GGGCCGCTGGGGCCACCTCCCTTTGCTTTGTTTACCCGCTGGACTTTGCTAGGACCAGG 420	01 GGGGTGTGGATCGGCATAAGCAGTTCTGGCGGTACTTTGCTGGTAACCTGGCGTCCGGT 360 	41 TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA 300 	81 ATCCCTAAGGAGCAGGGCTTCCTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT 240	21 GCCAGCAAACAGATCAGTGCTGAGAAGCAGTACAAAGGGATCATTGATTG	61 GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 120	1 ATGGGTGATCACGCTTGGAGCTTCCTAAAGGACTTCCTGGCCGGGGCGGTCGCCGCTGCC 60	h 79.7%; Score 712.4; DB 13; Length 1043; Similarity 97.8%; Pred. No. 2e-188; 44; Conservative 0; Mismatches 12; Indels 5; Gaps 2;	BM466452 Magnacourr_6431691 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:5503575 MRNA sequence. BM466452 BM466452 BM466452 BM466452.1 GI:18515494 EST. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1043) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. COMA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12143 row: i column: 16 High quality sequence stop: 744. Location/Qualifiers / Lone="Make:5503375" / Lione="Make:5503375" / Lone="IMAGE:5503375" / Lone="Make:5503375" / Lone="Make:550375" / Lone="Make:5503

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
cDNA Library Arrayed by: The I.M.A.G.E.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11652 row: a column: 19
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1 (bases 1 to 990)
NIH-MGC http://mgc.nci.nih.gov/.
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Location/Qualifiers
/clone_lib="IMAGE_95"
/clone_lib="IMAGE_95"
/tissue_type="hippocampus"
/lab.host="DHIOB"
/lab.host="DH
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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mRNA sequence.
BI408731
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18; Conservative
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Best Local
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                               TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA 300
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                         GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGT
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                   AGGCATGGGCGGTGCTTTTGTATTGGTGTTGTATGATGAGGATCAAAAAAT 886
                                                                                                                                                    GATTGCCAAAGATGAAGGAGCCAACGCTTTCTTCAAAGGTGCTTCGTCCAATGTACTGAG
                                                                                                                                                                                   GATTGCAAAAGACGAAGGAGCCAAGGCCTTCTTCAAAGGTGCCTGGTCCAATGTGCTGAG 836
                                                                                                                                                                                                                      GCAGTCTGGCCGGAAAGGGGCTGATATTATGTACACGGGGACACTTGACTGCTGGAGGAA
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                                                                                  AGGGCTTGGGTGCTTTGATGGCGATGGATTGAATGAGATCACAAACT 965
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REFERENCE AUTHORS ACCESSION VERSION DEFINITION JOURNAL ORGANISM Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium B1458368 879 bp m 603198738F1 NIH_MGC_96 Homo sapiens mRNA sequence Unpublished (1999) National Institutes of Health, 1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 879) Homo sapiens upunu BI458368.1 GI:15249024 Mammalian mRNA mRNA linear EST 21-AUG-2001 CDNA clone IMAGE:5278233 5', Gene Collection

SOURCE KEYWORDS

TITLE

FEATURES source e: LLAM11702 row: 1 column: quality sequence stop: 776. Locat

found through the I.M.A.G.E. Consortium/LLNL http://image.linl.gov

10

DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can

J. Brownstein (NHGRI), Shiraki

/clone_lib="NIH_MGC_96" /tissue_type="hypothalamus" /lab_host="DH108" /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5278233" on/Qualifiers

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692; Conserv
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12220 row: c column: 08
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AGENCOURT_6417828 NIH_MGC_71
5', mRNA sequence.
BM459526
BM459526 GI:18508566
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Tissue Procurement: ATCC
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National Institutes of Health, M
Unpublished (1999)
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1 (bases 1 to 882)
TCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGGTTGGCTGCTGATGTGGGC
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                                                                                                        AAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGTGGGGCCGCTGGGGCCACC
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5534143"
/clone_lib="NH_MGC_71"
/clone_lib="NH_MGC_71"
/lissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: pCMV-SPOR76; Site_Note="Organ: uterus; vector: pCMV-SPOR76; Site_Site_2: SalI; Cloned unidirectionally. Primer: Nverage insert size 2.1 kb.
a 208 c 241 g 229 t
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/db_xref="taxon:9606"
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RESULT 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nib.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI)
Toshiyuki and Piero Carninci (RTKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information
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1 (bases 1 to 907)
NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                               quality sequence stop: |
| Location/Qualifiers
                                                                                   for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

253 c 287 g 193 t
                                                                                                                                                             /note-"Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sal1-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                        /tissue_type="hypothalamus"
                                                                                                                                                                                                                                                                  /clone="IMAGE:5311319"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                          /lab_host="DH10B"
                         75.0%;
97.1%;
              0;
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Pred.
              ed. No. 1.1e-176;
Mismatches 16;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Tec
                                          Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 862)
                                                                                                                                                                                                            5', mRNA sequence
BQ214399
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AGENCOURT_7553137 NIH_MGC_68
                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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MAGE:6058078
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Plate: LLAM13322 row: i column:
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                   ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGGCAGTCGCAGGGCTGGTGGTCCTACCCCTTTGACACTGGNTCCGTCGTNAAATGATG
                          ACGGCAGTCGCAGGGCTGCT-GTCCTACCCCTTTGACACTG--TTCGTCGTAGAATGATG 714
                                                                                                          GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG
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/clone_lib="NIH_MGC_68"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH108 (phage=resistant)"
/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: Not1;
/note=2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies. "
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11353 row: a column: 13
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602987149F1 NCI_CGAP_Lu33 Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BI412906.1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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          ATCCCTAAGGAGCAGGGCTTCCTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT
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                                             cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11278 row: k column: 06 High quality sequence stop: 789.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 948)

NIH-MCC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                         mRNA sequence.
BI256359
BI256359.1 GI:14810692
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602975222F1 NIH_MGC_12
                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5114621"
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GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGCTCTACCCGCTGGACTTTGCTAGGACCAGG
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GAGGAAGATTGGAAAAGAGAAGGGGGGCAAGG
               GAGGAAGATTGCAAAAGACGAAGGAGCCAAG
                                                                  ATTGATGCAGTCCGGCGGAAAGGGGCCGATATTATGTACACGGGGACAGGTTGAATGGTG
                                                                                                                                      AGTGTGACGGCAGTCGCAGGGCTGCTGTCCTACCCCTTTGACACTGTTCGTCGTAGAATG
                                                                                                                                                                                                                                 ATGCTGCCTGACCCCAAGAACGT-GCACATTTTTGTGAGCTGGATGATTGCCCA-----G
                                                                                                                                                                                                                                                                                      GTCCAAGGCATCATTATCTATAGAGCTG · CTACTTCGGAGTCTATGATACTGCCAAGGGG
                                                                                                                                                                                                                                                                                                         GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG
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                                                                                                      ATGATGCAGTCCGGCCGGAAAGGGGCCGATATTATGTACACGGGGACAG-TTGACTGCTG
                                                                                                                                                                                                                  ATGCTGCCTGACCCCAAGAACGTGGCACATTTTTGTGAGCTGGATGATTGGCCAAGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI:
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Average insert size 1.4 kb. Library prepared Technologies."
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Pred. No. 1.3e-174;
0; Mismatches 40;
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420 504	361 GGGGCCGCTGGGGCCACCTCCCTTTCCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG	Оy
360 444	301 GGGGGTGTGGATCGGCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCGTCCGGT	. Db
300 384	241 TACTTCCCCACCCAAGCTCTCAACTTCGCCTTCAAGGACAAGTACAAGCAGCTCTTCTTA	Q Q V
240 324	181 ATCCCTAAGGAGCAGGGCTTCCTCTCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT	Οy
180 264	121 GCCAGCAAACAGATCAGTGCTGAGAAGCAGTACAAAGGGATCATTGATTG	Оy
120 204	61 GTCTCCAAGACCGCGGTCGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT	d dd Y
60	1 ATGGGTGATCACGCTTGGAGCTTCCTAAAGGACTTCCTGGCCGGGGGGGG	Оy
ω 	Ouery Match 73.8%; Score 659.4; DB 14; Length 946; Best Local Similarity 87.6%; Pred. No. 1.4e-173; Matches 755; Conservative 0; Mismatches 102; Indels 5; Gaps	Query Ma Best Loc Matches
11. GT.		SO ASE CO
	Ilssue procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the J.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13966 row: o column: 11 High quality sequence stop: 674.	FEATURES
	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	AUTHORS TITLE JOURNAL OMMENT
omi; Mus.	EST. house mouse. Nus musculus Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Rumanlia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 946)	KEYWORDS SOURCE ORGANISM
- 2002		DEFINITION ACCESSION VERSION

	Search completed: June 22, 2003, 04:08:45 Job time : 1086 secs	Search completed: Ju Job time : 1086 secs	Sea
	₹	925	Db
	GAGGCATGGGCGGTGCTTTTGT 857	836	Qy
924	AATGCCAAACAATTGAGGAGCCAACCGCTTTCTTCAAAGGGGCTTGGTCCCATGTACTGA 924	865	Дb
835	GATTGCAAAAGGAGGAGGGAGCCAA-GGCCTTCTTCAAAGGTGCCTGGTCCCAATGTGCTGA	777	Qy
864	GCAGCCTGGCCGGAAAGGGGCTGATATTATTTACACCGGGACACTTTACTGCTGCTGGAGGAA	805	Дb
776	GCAGTCCGGCCGGAAAGGGGCCCGATATTATGTACACGCGGGACAGTTGACTGCTGGAGGAA	717	Qy
804	ACAACGGTGGCCGGGGCTGGTCCTATCCGTTTGACACTGTTCGTCGTAAGATGATGAT	745	ДĎ
716	ACGGCAGTCG-CAGGGCTGCTGTCCTACCCCCTTTGACACTGTTCGTCGTCGTAGAATGATGAT	658	Oy
744	ATGCTGCCAGACCCCAAGAATGTGCACATTATCGTGAGCTGGATGATTGCCCCANAGTGTG	685	ДĎ
657	ATGCTGCCTGACCCCAAGAACGTGCACATTTTTGTGAGCTGGATGATTTGCCCAGAGTGTG	598	Qy
684	GTCCAGGGCATCATCTACAGAGCTGCCTACTTCGGAGTCTATGACACTGCCAAGGGG	625	Db
597	GTCCAAGGCATCATTATCTATAGAGCTGCCTACTTCGGAGTCTATGATACTGCCAAGGGG	538	Qy
624	CTCACCAAGATCTTCAAGTCGGACGGCCTGAAGGGTCTCTACCAGGGTTTCAGTGTCTCTCT	565	Db
537	ATCATCAAGATCTTCAAGTCTGATGGCCTGAGGGGGCTCTACCAGGGTTTCAACGTCTCT	478	Оу
564	CTGGCTGCCGACGTGGGCAAGGGATCTTCCCCAGCGAGAATTCAATGGGCTGGGCGACTGT	505	Db
477	TTGCCTGCTGATGTGGGCAGGCGCG	421	. Oy